



Supplementary Materials for

MicroRNA-128 governs neuronal excitability and motor behavior in mice

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Materials and Methods

Animals

Mice were housed at two to five animals per cage with a 12-hour light/dark cycle (lights on from 0700 to 1900 hours) at constant temperature (23 °C) with *ad libitum* access to food and water. All animal protocols were approved by IACUC at The Rockefeller University, The Northwestern University, and Icahn School of Medicine at Mount Sinai.

Generation of Mice

Generation of mice with a conditional deletion of *miR-128-1* and *miR-128-2*:

Subcloning of targeting vectors: A region of the *miR-128-1* or *miR-128-2* genomic locus containing the arms of homology was recombinogenically subcloned from a BAC clone (*mir128-1*: RP24-574G14, *miR128-2*: RP24-242F13, C57Bl/6J, CHORI, Oakland CA, USA) into pBlueScriptIIKS+ using amplicons that insert an AscI site and a XhoI site to flank the subcloned region.

PCR primers used for subcloning:

mir-128-1

5' cttcatgttatgcctcatccattatcacacaatctgttagtttcggcgccatcgccatagtgagtcg

5' aatctctaaattccatttgaggcacctagttcatatgaatttagattcctcgaggcttggcgtaatcatggc

mir-128-2

5' cgaaaaatatttcatttattctcgaaacttcatacattatacatgtggcgccatcgccatagtgagtcg

5' tcaggcctgccagcctctgtctactgttaatgactgacagccagtgaactcgaggcttggcgtaatcatggc

*Modification of targeting vector for *miR-128-1*:*

pZeroLoxP-FRT-neoR-FRT(-) was modified to replace the unique EcoRI site with a unique SmaI site. The following oligonucleotide fragments were annealed and inserted into the EcoRI site:

5' aattgcatcgcatgggtcacgacgagatccggggc

5' aattgcccggatctcgatccccatgcgatgc

The modified plasmid was digested with NsiI, and the fragment containing a single loxP site and the FRT-flanked *neo* gene was inserted into the unique NsiI site in the targeting vector and screened for proper orientation. For insertion of the second loxP site, the following oligonucleotide fragments were annealed and inserted into the unique SpeI site:

5' ctagaataacttcgtatgcatacattatacgaagtttatgaattct

5' ctagagaattcataacttcgtataatgtatgctatacgaagttatt

Modification of targeting vector for miR-128-2

pZeroLoxP-FRT-neoR-FRT(-) was modified by digesting the plasmid with SacI and ApaI and annealing and inserting the following oligonucleotide fragments:

5' ggaaggttcctatacttctagagaataggaacttcggaataggaacttcagagctcatcgagcccccgttagacggcccc

5' gtctaccgggctcgatgagctctgaaggttcctattccgaaggttcctattctctagaaagtataggaacttccagct

The plasmid was further digested with Acc65I and the following oligonucleotides were annealed and inserted:

5' gtaccccccggataacttcgtatagcatacattatacgaagttataagcttc

5' gtacgaagctataacttcgtataatgtatgctatacgaagttatcccgcccc

The modified plasmid was digested with SmaI and the fragment containing a single loxP site and the FRT-flanked *neo* gene was inserted into the unique SmaI site in the targeting vector and screened for proper orientation. For insertion of the second loxP site, the following oligonucleotides were annealed and inserted into the unique HindIII site:

5' agctaataacttcgtatagcatacattatacgaagttatggatcct

5' agctaggatccataacttcgtataatgtatgctatacgaagttatt

For both targeting vectors, the modified regions of homology were excised from pBluescript with XhoI and AscI digests and inserted into similarly digested pDTA-TK to produce the final targeting constructs. The targeting constructs were linearized with NotI, and E14 CY2.4 embryonic stem cells (homozygous C57Black/6JTyr-C-2J background with natural mutation in tyrosinase gene) were transfected and screened for successful recombination using a Southern probe. Positive clones were confirmed using an alternate Southern probe and by PCR sequencing of the modified region. Positive clones were used

to produce chimeric mice as described. Chimeras were crossed to C57BL6/J mice, and germline transmission was assessed by coat color, PCR and Southern blot analysis. Germline deletion of the FRT-flanked *neo* gene was accomplished by crossing mice carrying the targeted alleles with FLPe- transgenic mice (Jackson Laboratory). Germline deletion of *miR-128-1* and *miR-128-2* to generate *miR-128-1^{-/-}* and *miR-128-2^{-/-}* mice was achieved by crossing mice carrying floxed alleles to transgenic mice that express Cre-recombinase driven by the ubiquitously expressed *CMV* promoter (*CMV-cre* mice, Jackson Laboratory).

Postnatal, neuron-specific deletion in the mouse forebrain was achieved by breeding mice carrying floxed alleles (*miR-128-2^{f/f}*) to *Camk2a-cre* mice (31) to generate *Camk2a-cre; miR-128-2^{f/f}* mice. *Drd1a-cre* (EY262) and *A2a-cre* (KG139) transgenic mice were obtained from Gensat (32) and crossed with *miR-128-2^{f/f}* to generate *Drd1a-cre; miR-128-2^{f/f}* and *A2a-cre; miR-128-2^{f/f}* mice.

Routine genotyping of *miR-128-1* mice was performed using following primers:

5'-tctggaccaaattgaaaccaaag

5'-ccgcaatgcgtgccttatattc

5'-gcctgaagaacgagatcagc

5'-gcagtcatgcaaggcagctat

Wild type allele: 194bp

Null allele: 282bp

Floxed allele: 336bp

Routine genotyping of *miR-128-2* mice was performed using following primers:

5'-cgcctttagttcccacag

5'-gaccacacagcaaggcaggt

5'-aaagacgggaccattcacat

5'-tctctcgatggatcattgttt

Wild type allele: 185bp

Null allele: 531bp

Floxed allele: 306bp

Generation of mice with a neuron-specific overexpression of *mir-128-2*.

The targeting vector for homologous recombination at the *ROSA26* locus was generously provided by K. Rajewsky (30). A 1kb region including miR-128-2 hairpin was amplified from genomic DNA with the following primers and cloned into the unique XhoI site in the targeting vector:

5' aaaggcgccacgtgACTAAAAGGCGCGAGGAGAT

5' aaaggcgccTACGCATTCTGTACGGTTG

Modified targeting vector was linearized by NotI and used to generate chimeras as above. Successful germline transmission was assessed by coat color and confirmed by PCR and Southern analysis. Routine genotyping of *Rosa-miR-128* mice was performed using the following primers:

5'-gagttctctgctgcctcctg

5'-ggaaagtccctattggcgat

5'-tgctgcataaaaccccagat

Wild type allele: 292 bp

Rosa-miR-128 targeted allele: 408 bp

Postnatal, neuron-specific miR-128-2 overexpression in the mouse forebrain was achieved by breeding homozygous *Rosa-miR-128* mice to *Camk2a-cre* mice (31) to generate *Camk2a-cre; Rosa-miR-128* mice. *Rosa-miR-128* mice were bred to *Camk2a-cre; miR-128-2^{f/f}* mice to generate *Camk2a-cre; miR-128-2^{f/f}; Rosa-miR-128* rescue mice.

Generation of mice with neuron-specific FLAG tagged-Ago2 expression:

Transgenic mice expressing a Cre-inducible FLAG-HA2-tagged Ago2 under the control

of the *ROSA26* promoter were generated as previously described (9, 30). The *STOP-eGFP-ROSA26TV* vector was a gift from K. Rajewsky, Harvard Medical School, Boston, MA. *Rosa-Stop^{f/f}-Flag-Ago2* mice were bred to *Camk2a-cre* transgenic mice (kindly provided by G. Schuetz, German Cancer Research Center, Heidelberg, Germany (31)) to generate *Camk2a-cre; Rosa-Stop^{f/f}-Flag-Ago2* mice.

Camk2a-neuron specific RISC-associated RNA isolation and analysis

In vivo Crosslinking and Immunoprecipitation (CLIP) procedure.

In three independent experiments (experiment 1-3), mice that express a Flag-tagged Ago2 protein specifically in Camk2+ neurons in the forebrain (*Camk2a-cre; Rosa-Stop^{f/f}-Flag-Ago2*) and control mice (*Rosa-Stop^{f/f}-Flag-Ago2*) were sacrificed at 8 to 14 weeks of age. Forebrains were excised, triturated to disrupt tissue, and UV-irradiated three times in a Stratalinker with 400mJ/cm². Immunoprecipitation was performed as described (8) with the following modifications to the protocol: After UV crosslinking the frozen lysates were sonicated to improve tissue homogenization. RNase digestion with RNase A was performed before IP (using one fourth the concentration of RNase A used by (8)), and after IP (using one twentieth the concentration of RNase A used by (8)). 30µl of magnetic beads pre-coupled to the M2 FLAG antibody (M8823, Sigma) were used for IP on half of one forebrain after pre-blocking the beads with 2% BSA, 1% t-RNAs and 1% salmon sperm for 1.5 hrs at 4°C. RNA was directly de-crosslinked from protein after extensive washing.

Illumina Sample Preparation and Sequencing.

The small RNA sample preparation kit, version 1.5 (Illumina), was used for library preparation with subtle modifications. Because low concentrations of RNA were purified from the CLIP procedure, as measured by Quant-iT RiboGreen RNA Assay (Invitrogen), the following modifications were made to the small RNA sample preparation kit (Illumina) to allow for low RNA input: Both the v1.5 sRNA 3' Adapter and the SRA 5' Adapter were diluted 10 times in nuclease-free water compared to the standard protocol before adapter ligation. The RT reaction was doubled (resulting in a final RT volume of 20 µl instead of the standard 10 µl), all of which was used for the downstream PCR

reaction. To allow for the larger volume of RT product, 10 µl less water was used in the PCR step, resulting in a final PCR volume of 50 µl. Instead of the 12 cycles of PCR directed in the standard protocol 15 cycles were performed to increase output.

RNA from four CLIP procedures were pooled for each library preparation, amounting to CLIP RNA from two mouse forebrains per library. At the end of the Illumina small RNA protocol, the products were purified from a gel at the size of 110 to 150 bp, containing adapter-linked RISC-associated mRNA target sites.

Prepared samples were amplified onto flow cells using the Illumina cluster station per manufacturer protocol and sequenced on the Illumina GAIIx platform for 76 cycles. Raw sequencing data was processed using the onboard SCS/RTA software.

Pre-processing of sequencing data

All sequence reads were trimmed by quality from both ends, removing any base with a quality score of less than 20. Next, reads were filtered to remove low quality reads, using a minimum average cutoff quality score of 20 over 90% of the read. Sequence reads were trimmed of any identifiable adapter sequence, and reads of at least 24 bases were used for mRNA target analysis. These reads were aligned to the current mouse genome (mm10) using bwa (Burrows-Wheeler Aligner) (33) with default settings for mismatch limits.

Aligned reads of three independent experiments:

1,826,496	Control #1
2,889,818	Flag-Ago2 #1
15,555,118	Control #2
9,853,284	Flag-Ago2 #2a
8,634,607	Flag-Ago2 #2b
8,938,571	Control #3
9,443,923	Flag-Ago2 #3a
7,405,866	Flag-Ago2 #3b

Detection of mRNA target sites clusters:

For the downstream analysis of mRNA targets, RISC-associated RNA reads were filtered and clustered to allow detection of mRNA target sites. Data processing is described below and shown as a flow chart in Fig. S5A. To reduce contributions of nonspecifically binding RNA species from cluster detection, any RISC-associated RNA read within 35 bp of 5 or more overlapping reads from the grouped control samples were discarded. Only reads occurring in at least two-filtered Flag-Ago2 samples were kept, and 30 nucleotides of genomic sequence was added to each end of the filtered reads. These reads were filtered to only retain clusters composed of minimum 10 overlapping reads. Filtering resulted in detection of 70,832 clusters. Genomic distribution of clusters was examined by use of Cis-regulatory Element Annotation System (CEAS) (34). Filtered clusters that specifically intersect with RefSeq 3'UTR plus 1 kilobase additional downstream genomic sequence (3'UTR+1kb) were used for MEME-ChIP analysis, 6mer analysis and genome-wide target site analysis.

MEME-ChIP analysis:

Enriched sequence motifs were detected by the motif discovery software, MEME-ChIP (35). The sequences of Ago2-CLIP clusters in the 3'UTR+1kb region of RefSeq genes (n=8794) were used as input for MEME-ChIP. A Markov background model was made from all 3'UTR+1kb regions in RefSeq and used with MEME-ChIP to allow detection of motifs enriched over the relevant background. Motifs were searched specifying that zero or one occurrence of a motif is present in each cluster sequence, the ‘zoops’ option. Otherwise, the default settings were used for the analysis.

6mer analysis:

The abundance of all possible 6mer sequences was found using the perl script countkmer.pl (by Marco Blanchette) on the sequences of Ago2-CLIP clusters in the 3'UTR+1kb region of RefSeq genes (n=8794). The same was done for all RefSeq 3'UTR+1kb genomic sequences to use as background (normalized to contain the same total number of 6mers as detected in clusters). The z-score and chi-square p-value were

calculated for all 6mer sequences enriched in clusters over RefSeq 3'UTR+1kb genomic sequences. The z-score was calculated for each 6mer by subtracting the abundance in RefSeq (background) from the abundance in clusters and subsequently dividing by the standard deviation of the background subtracted abundance of all 6mers. The value of the z-score conveys the distance from the mean for a given 6mer in units of standard deviation of the entire collection of 6mers.

Genome-wide target site analysis:

Bowtie (36) was used to map all occurrences of sequences complementary to the 6mer seed sequence of miR-128 in the mouse genome mm10, allowing no mismatches. Strand specific intersection was done with the filtered clusters in the 3'UTR+1kb RefSeq region, generating a genome-wide list with predicted miR-128 target sites.

RNA Preparation

Mice were anesthetized with CO₂, and the respective brain regions or peripheral organs were rapidly dissected and frozen in liquid nitrogen until further processing. RNA extraction from frozen samples was performed using the TRIzol/Chloroform technique according to manufacturer's instructions (Invitrogen Corporation, Carlsbad, CA). After extraction, RNA was precipitated overnight at -80C in isopropanol with 0.15M sodium acetate, washed twice with 70% ethanol, air-dried, and resuspended in RNase-free water.

D1-neuron specific TRAP analysis

Mice with D1-neuron specific loss of miR-128-2 (*Drd1a-cre; miR-128-2^{f/f}*) were crossed to mice carrying D1-MSN specific expression of eGFP-tagged ribosome protein L10 ((11), *D1-TRAP*). Polyribosome-associated mRNAs from 6 week old, age- and sex-matched *Drd1a-cre; Drd1a-TRAP; miR-128^{f/f}* and *Drd1a-TRAP; miR-128^{fl/fl}* mice (n=5/genotype) were obtained as previously described (11). eGFP-labeled ribosomes and associated mRNAs were immunoprecipitated using a mix of two monoclonal anti-GFP antibodies (50 µg of clones #19C8 and #19F7 for each IP, available at Sloan-Kettering Monoclonal Antibody Facility). Purified mRNA was amplified and processed for microarray and qPCR analysis using the Affymetrix two-cycle cDNA Synthesis kit

(Affymetrix, Santa Clara, CA) as previously described (11). Affymetrix Mouse Genome 430 2.0 arrays were used in all experiments. Information regarding the array design and features can be found at www.affymetrix.com. Mouse Genome 430 2.0 arrays were scanned using the GeneChip Scanner 3000 (Affymetrix, Santa Clara, CA) and globally scaled to 150 using the Affymetrix GeneChip Operating Software (GCOS v1.4). GeneChip files (.cel) were imported into GeneSpring software (Agilent Technologies, Santa Clara, CA) and processed with RMA algorithm, and expression values on each chip were normalized to median of all samples. D1-neuron specific ribosome-associated mRNAs from two independent experiments were analyzed. All probes with differential expression and p-value ≤ 0.05 using 2-way ANOVA (genotype) were considered significantly changed in the absence of miR-128-2.

Dataset from TRAP experiments were analyzed by SYLAMER algorithm to determine if miR-128 targets were more abundant among genes upregulated in the absence of miR-128 compared to genes downregulated in the absence of miR-128. Genes on the array were ranked from most upregulated to most downregulated genes in *Drd1a-cre; Drd1a-TRAP; miR-128^{fl/fl}* as compared to *Drd1a-TRAP; miR-128^{f/f}* mice according to fold-change t-statistic. The enrichment analysis was obtained by SYLAMER with Bonferroni-corrected p-value threshold of 0.05 (<http://www.ebi.ac.uk/enright-srv/sylarray/>).

TaqMan Quantitative RT-PCR for miRNA and mRNA analysis

Relative expression levels of mature miRNAs and mRNAs were measured by TaqMan assays using total extracted RNA from brain samples, according to manufacturer's protocol (Life Technologies, Carlsbad, CA). Purified RNA samples were assayed by qRT-PCR for relative gene expression using pre-designed TaqMan gene expression assays from Applied Biosystems (ABI) as recommended by the manufacturer. The following pre-designed TaqMan gene expression assays from Applied Biosystems (ABI) were used: miR-128 (Assay ID 002216), sno135 (Assay ID 001230), miR-124a (Assay ID 001182), Fosb Mm00500401_m1, Fosl2 Mm00484442_m1, Arc Mm00479619_g1, JunB Mm04243546_s1, Darpp-32 Mm00454892_m1, Btg2 Mm00476162_m1, Gadd45g Mm01352550_g1, Dusp1 Mm00457274_g1, Nr4a1 Mm01300401_m1, Jun Mm00495062_s1, Actb Mm00607939_s1, Arpp-21 Mm00473630_m1 (exon spanning

probe detects exons that are common to all Arpp-21 isoforms), Arpp21 Mm00473645_m1 (exon spanning probe that specifically detects the long TARPP-isoform of Arpp-21). Cycle counts for miRNA quantification were normalized to snoRNA135 or miR-124a as indicated, and cycle counts for mRNA quantification were normalized to Actb or Gapdh. Relative expression (ΔCt) and quantification ($RQ=2^{-\Delta Ct}$) for each mRNA were calculated using RQ Manager Software and the $\Delta\Delta Ct$ method as suggested. Calculation of standard deviation ($SD_{\Delta Ct}=(SD_{target}^2+SD_{ref}^2)^{1/2}$) and error bars ($RQ_1=2^{(-(\Delta\Delta Ct+SD_{\Delta\Delta Ct}))}$, and $RQ_2=2^{(-(\Delta\Delta Ct-SD_{\Delta\Delta Ct}))}$) was performed according to ABI technical literature Part Number 4371095 Rev B.

Pathway analysis

Bioinformatic network and pathway analyses of the 154 miR-128 target genes was performed using IPA (Ingenuity Systems, Redwood City, CA) and the Database for Annotation, Visualization and Integrated Discovery (DAVID) version 6.7 (david.abcc.ncifcrf.gov/).

Protein Preparation and Expression Analysis

Mice were anesthetized with CO₂ and the cortex, hippocampus, and striatum were rapidly dissected and frozen in liquid nitrogen until further processing. Samples were sonicated on ice in 1% SDS solution supplemented with protease inhibitor (Roche, Switzerland) and phosphatase inhibitor, and boiled for 10 minutes. Protein concentration was determined using BCA protein assay kit (ThermoFisherScientific, USA) according to the manufacturer's instructions. Protein samples were diluted in equal volume of 2X LDS sample buffer (Invitrogen) and supplemented with DTT to a final concentration of 200mM (Sigma). 25ug of protein samples were separated on 4-12% Bis-tris precast denaturing gels (Invitrogen), transferred onto PVDF membranes, and blocked with 5% milk in TBS- 0.1% Tween (TBST) solution for 1 hour at room temperature. Membranes were probed with primary antibodies diluted in 5% milk-TBST solution overnight at 4C. Membranes were then washed and probed with horseradish-peroxidase conjugated anti-mouse (GE) or anti-rabbit IgG secondary antibody (GE) for 1 hour at room temperature. Membranes were developed using enhanced chemiluminescence substrate (PerkinElmer,

USA) and exposed on BioMax film (Kodak, USA). Exposed films were scanned, and protein bands were quantified using ImageJ Software (NIH, USA). Protein quantities were normalized using beta-Actin, phosphoprotein levels were normalized to total non-phosphorylated protein levels, and all values plotted relative to control littermate sample. The following primary antibodies were used: total ERK1/2 (137F5), phosphoERK1/2 (Thr202/Tyr204), Arpp21 (mouse monoclonal 6A, gift. A. Nairn), beta-Actin (Abcam), PEA15a (H80) (Santa Cruz,), D4ertd22e (Atlas).

ELISA Assay

The ELISA quantification was performed using the PathScan MAP kinase Multi-Target Sandwich ELISA kit (Cell Signaling) according to manufacturer's instructions. Briefly, tissue samples were dissected and rapidly frozen in liquid nitrogen before further processing. Frozen samples were lysed in cell lysis buffer with brief sonication on ice. Cell lysate was centrifuged at 14,000 rpm for 10 min, and the supernatant was diluted 1:10 in sample diluent and used for incubation with antibody micro-wells according to the manufacturer's protocol. Standard curves were generated using dilutions of a mixture containing equal proportion of all control samples. Relative quantity of total or phosphorylated MAP kinase pathway proteins in *Drd1a-cre; miR-128-2^{f/f}* and control striatum lysates were quantified based on the individual absorbance values at 450nm. The p-values were calculated using the Welch's test.

Luciferase Reporter Assay

Luciferase reporter assays were performed to measure the repression of RCS and TARPP mRNA expression by miR-128. MicroRNA 3'UTR target reporter plasmids that contain the full length sequences of the RCS and TARPP 3'UTR downstream of a firefly luciferase gene driven by a *SV40* promoter for expression in mammalian cells were purchased from GeneCopoeia, MD (pEZX-MT01). Control plasmids containing no 3'UTR inserts were used for comparison. Plasmids contain the Renilla luciferase gene to control for transfection and expression efficiency. The sequences of all plasmids were verified by sequencing and restriction enzyme digestion. Reporter or control plasmids were co-transfected with the Renilla luciferase plasmids into confluent Neuro2A cells

grown in 24-well culture plates with either no miRNA mimic, a miR-124a scrambled control mimic, or miR-128 mimics at the two indicated concentrations (Dharmacon, Thermo Fisher Scientific, USA). Cells were harvested and lysed 24 hour after transfection and cell lysates were assayed for firefly and Renilla luciferase activity using Dual-Luciferase Reporter Assay System (Promega, Wisconsin, USA) according to manufacturer's instructions. Firefly luciferase activity was normalized to Renilla luciferase activity for each cell culture well and plotted as activity relative to control transfections with no mimics added. At least 3 biological replicates were performed consisting of 3 technical replicates each.

Electrophysiological Analysis

Brain slice preparation:

Para-sagittal brain slices (275 μm) were obtained from 3-5 month old male and female *Drd1a-TRAP*; *Drd1a-cre*; *miR-128^{f/f}* and *Drd1a-TRAP*; *miR-128^{fl/fl}* littermate control mice following procedures approved by the Northwestern University Institutional Animal Care and Use Committee. The mice were anesthetized with a mixture of ketamine (50 mg kg^{-1}) and xylazine (4.5 mg kg^{-1}) and perfused transcardially with 5–10 ml ice-cold artificial cerebrospinal fluid (ACSF) containing (in mM): 124 NaCl, 3 KCl, 1 CaCl_2 , 1.5 MgCl_2 , 26 NaHCO_3 , 1 NaH_2PO_4 , and 16.66 glucose, continuously bubbled with carbogen (95% O_2 and 5% CO_2). The slices were then transferred to a holding chamber where they were incubated in ACSF containing (in mM) 2 CaCl_2 , 1 MgCl_2 , at 35°C for 60 min, after which they were stored at room temperature until recording.

Electrophysiology:

Patch pipettes were pulled from thick-walled borosilicate glass on a Sutter P-97 puller. Pipette resistance was typically 3–5 $\text{M}\Omega$ when filled with recording solution. For studies involving bAP propagation, the internal recording solution contained (in mM): 135 KMeSO₄, 5 KCl, 10 HEPES, 2 ATP-Mg²⁺, 0.5 GTP-Na⁺, 5 phosphocreatine-tris; 5 phosphocreatine-Na⁺, and 0.1 spermine. The pH was adjusted to 7.25 with NaOH and osmolarity to 270–280 mOsm l^{-1} . For Ca²⁺ imaging experiments, the recording solution also contained 200 μM Fluo-4 pentapotassium salt and 50 μM Alexa Fluor 568 hydrazide

Na^+ salt (Invitrogen). For voltage clamp studies, the recording solution contained (in mM): 120 CsMeSO₃, 5 NaCl, 10 TEA-Cl (tetraethylammonium-Cl), 10 HEPES, 5 Qx-314, 4 ATP-Mg₂, 0.3 GTP-Na, 0.2 Fluo 4 pentapotassium salt and 0.05 Alexa Fluor 568 hydrazide Na^+ salt (Invitrogen), pH 7.25, 270–280 mOsm⁻¹. Slices were transferred to a submersion-style recording chamber mounted on an Olympus BX51 upright, fixed-stage microscope and continuously perfused with carbogen-bubbled ACSF. Electrophysiological recordings were obtained with a Multiclamp 700B amplifier. Stimulation and display were obtained as previously described (Day et al., 2008) using the custom-written shareware package WinFluor (John Dempster, Strathclyde University, Glasgow, Scotland, UK), which automates and synchronizes the two-photon imaging and electrophysiological protocols. The amplifier bridge circuit was adjusted to compensate for serial resistance and continuously monitored during recordings.

2-photon laser scanning microscopy (2PLSM) and Ca^{2+} imaging:

2PLSM and Ca^{2+} imaging were performed as previously described (37). Striatonigral spiny projection neurons (SPNs) were identified by somatic eGFP two-photon excited fluorescence using an Ultima Laser Scanning Microscope system (Prairie Technologies). A DODT contrast detector system was used to provide a bright-field transmission image in registration with the fluorescent images. The green GFP signals (490–560 nm) were acquired using 810 nm excitation (Verdi/Mira laser). SPNs were patched using video microscopy with a Hitachi CCD camera and an Olympus 60X/0.9 NA lens. Alexa 568 fluorescence was used for visualization of cell bodies, dendrites, and spines. Following patch rupture, the internal solution was allowed to equilibrate for 15–20 minutes before imaging. High magnification maximum projection images of dendrites were acquired with 0.072 μm^2 pixels with 10 μm pixel dwell time. Approximately 20 images taken with 0.5 μm focal steps. Spine density was calculated from maximum projection images of dendritic segments ~100–120 μm from the soma, as previously described (38). Spines were manually counted and normalized to the length of the corresponding dendrite.

Single bAPs were generated by injecting somatic current pulses (2 nA, 2 ms). Dendritic changes in Ca^{2+} were measured as $\Delta F/F_0$ via line scans, where F_0 is the average green fluorescence before the bAP. Peak $\Delta F/F_0$ values were obtained from the average of 6

consecutive trials and calculated by a single exponential fit of the Ca^{2+} transient decay. Green fluorescent line scan signals were acquired at 6 ms per line and 512 pixels per line with 0.08 μm pixels and 10 μs pixel dwell time. The laser-scanned images were acquired with 810 nm light pulsed at 90 MHz (\sim 250 fs pulse duration). Power attenuation was achieved with two Pockels cells electro-optic modulators (models 350–80 and 350–50, Con Optics, Danbury, CT). The two cells were aligned in series to provide an enhanced modulation range for fine control of the excitation dose (0.1% steps over four decades). The line scan was started 200 ms before the stimulation protocol and continued 4 s after the stimulation to obtain the background fluorescence and to record the decay of the optical signal after stimulation. To reduce photo-damage and photo-bleaching, the laser was fully attenuated using the second Pockels cell at all times during the scan except for the period directly flanking the bAP burst. Dendritic line scans were acquired from proximal (\sim 50 μm from soma) and distal (\sim 100-120 μm from soma) dendritic regions for each cell. bAP attenuation was calculated by normalizing distal Ca^{2+} transient peaks to the maximum proximal Ca^{2+} transient per cell.

Glutamate uncaging was achieved using a Chameleon-XR laser system (Coherent Laser Group, Santa Clara, CA). 5 mM MNI-glutamate (Tocris, Cookson, Ellisville, MO) was superfused over the slice using a syringe pump and multi-barreled perfusion manifold (Cell MicroControls, Norfolk, VA). Glutamate was uncaged adjacent to individual spine heads using 1 ms pulses of 720 nm light typically 10-20 mW in power at the sample plane. Photolysis power was tuned via a third Pockels cell modulator (Con Optics, Danbury, CT) to achieve uncaged-EPSCs (uEPSCs) averaging 5-10 pA.

Behavioral analysis

For all behavioral experiments, experimenters were blinded to the genotypes of the animals. All behavior tests have been performed on 4- to 16-week-old mutants and their respective age- and sex-matched littermate controls. All behavior tests were conducted between 7 AM and 7 PM. Genotypes were decoded after data was processed and analyzed. Sample sizes of at least 5 animals were used for behavioral analyses. Subjects corresponding to data points that are more than 2 standard deviations from the sample mean were excluded from analyses. When possible, all littermate animals were included

in behavioral experiments as control groups. No randomization protocol was used. Animals were allocated to treatment groups to ensure uniform distribution of ages and sexes in each group. Where 2 conditions are compared, 2-tailed Welch's t-test was used. For comparisons involving multiple sample groups, either 1-way or 2-way ANOVA was used. When a factor had a significant effect, post-tests were performed for pairwise comparisons.

Open-Field Analysis:

Locomotion and exploratory behavior was measured using the open field (40 X 40 X 30 cm). Activity was quantified by the computer-operated Photobeam activity system (Accuscan Instruments, Columbia, OH). Mice were recorded for total distance moved in the whole arena and number of vertical episodes (rearing). Open field analysis was performed on 4 week old mice and their respective age and sex-matched littermate controls. To ensure that the experimental mice had no seizures at the time of the analysis, the mice used for the behavioral tests were kept under surveillance for 2 hours prior to the test, during the 1-hour motor test, and 4 hours after the test.

Drugs used:

Mice were injected intraperitoneally (i.p.) with the microliter volume equivalent of 10X body weight (g). D1-receptor agonist SKF 81297 (Taconic) was diluted from stock (10mg/ml in DMSO) with 0.9% saline to indicated concentration. MEK inhibitor SL327 (Taconic) was diluted from stock (diluted in DMSO) with 30% DMSO/Saline to indicated concentration. Cocaine (Sigma, C5776) was diluted in water to a 100mg/ml stock solution. Sodium valproate (Sigma, P4543) was prepared at a 0.26% w/v solution in drinking water for oral administration. Kainic acid (Sigma, K0250) was dissolved in saline just before use to 30mg/kg concentration for i.p. injections. Picrotoxin (Sigma, P1675) was prepared as a 25mg/ml stock solution in ethanol and further diluted in saline to inject at a 3mg/kg concentration for seizure induction.

Home Cage Seizure Monitoring:

Animals were housed in clear plexiglass chambers with pre-installed cameras

(Phenotyper, Noldus Information Technology), and provided with food and water *ad libitum*. Continuous 24-hour video recordings of mice were taken. Video recordings were manually scored for severity, duration and frequency of seizures. To constitute recorded tonic-clonic seizures, mice must cease all normal activity such as walking, sniffing or grooming, adopt a rigid posture with arched back and progress to repeated rearing and falling. A large majority of tonic-clonic seizure episodes progressed to a further stage with rapid running and bouncing behavior, although this was not required for inclusion as tonic-clonic seizure.

Chemically-induced seizures:

Mice were injected i.p. with kainic acid (30 mg/kg in saline) or picrotoxin (3 mg/kg in saline) and placed in chambers in isolation and observed for 60 min. after injection. All injected animals rapidly enter period of immobility (Stage 1). Animals were observed for the time of onset of tonic-clonic seizures characterized by repeated rearing and falling followed by running and bouncing, or constant limb movements if postural control is lost.

Survival curves:

Date of sacrifice or death in the home cage was recorded for mutants and cage mate controls, plotted as Kaplan-Meier survival curves, and compared using log-rank tests.

6-OHDA lesions:

Mice were anesthetized with ketamine/xylazine. Mice were stereotactically injected with 6-OHDA (3.5mg/ml in 0.02% ascorbic acid) 2X2ul in left striatum (ML=-2.1 AP=+1.0 DV=-3.4; ML=-2.3 AP=+0.3 DV=-3.4) and vehicle injection 2X2ul in right striatum (ML=+2.1 AP=+1.0 DV=-3.4; ML=+2.3 AP=+0.3 DV=-3.4). Mice were single housed for 3 weeks after surgery to allow for recovery before behavioral assays.

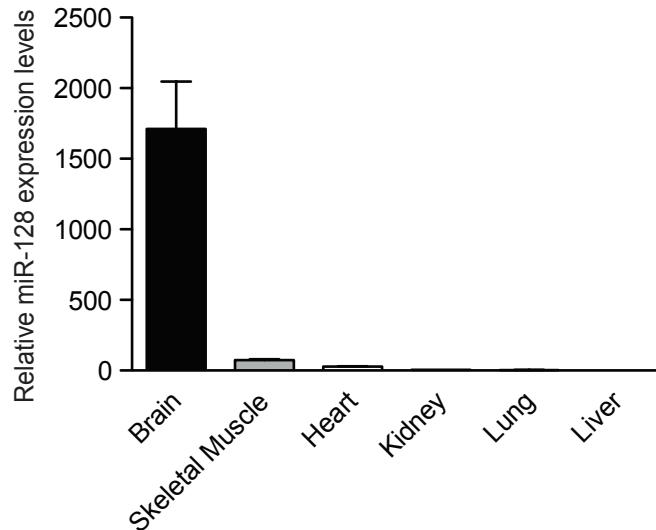
Rotational behavior:

Rotational behavior in lesioned mice was assayed by an experimenter blind to the genotypes for two consecutive 2-min intervals 5 min after i.p. injection of cocaine. Net contralateral rotations are given by total contralateral rotations minus ipsilateral rotations.

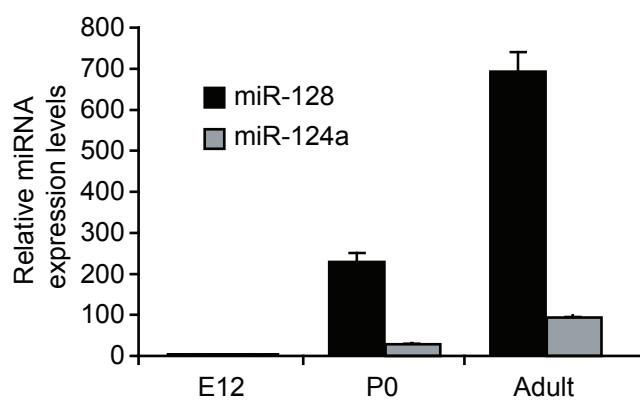
Data shows average of both readings. After 3 days, the same behavioral assay was recorded in response to SKF81297.

Figure S1.

A



B



C

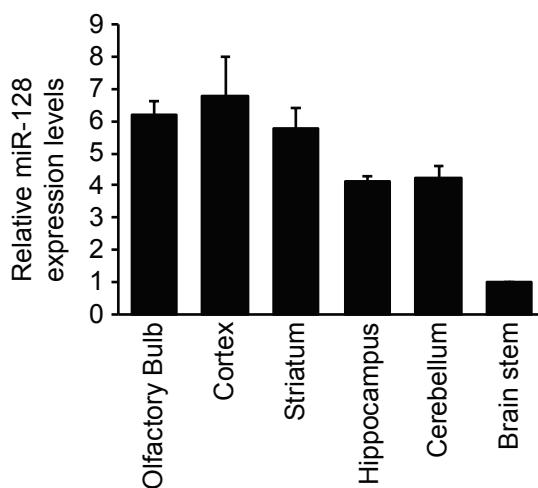
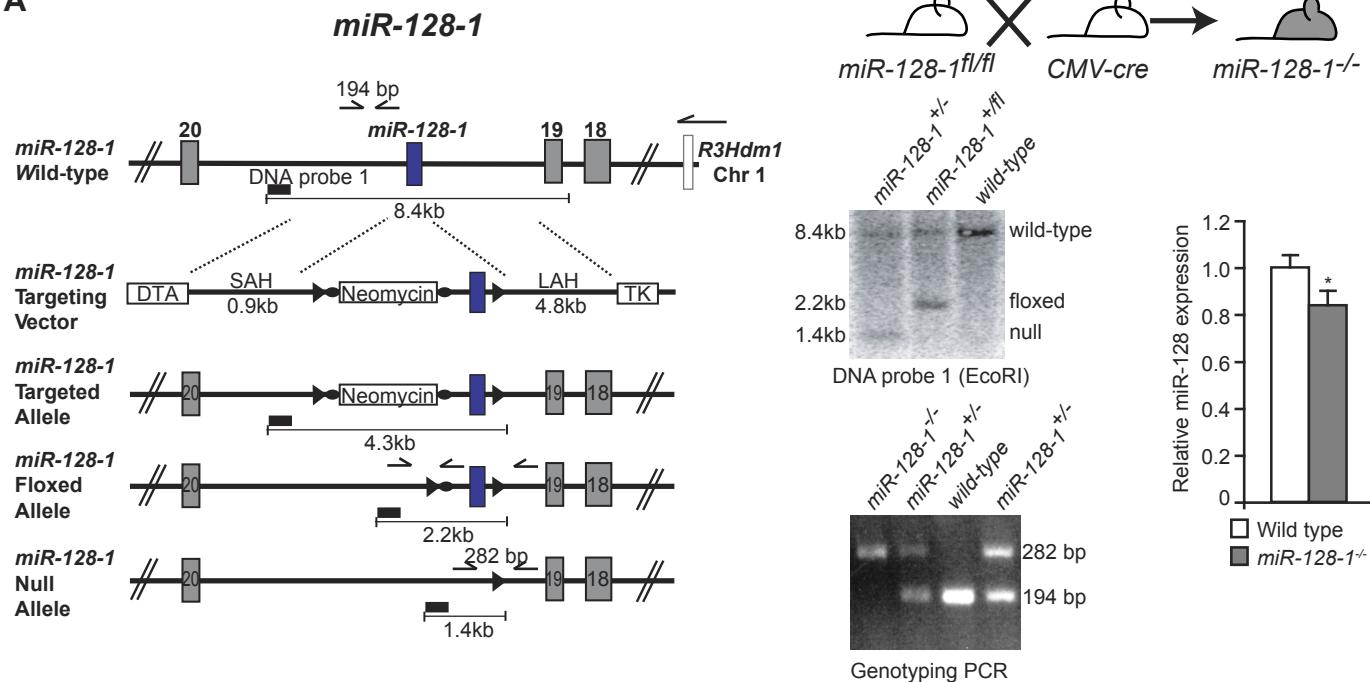


Figure S1. miR-128 is highly expressed in the postnatal mouse brain.

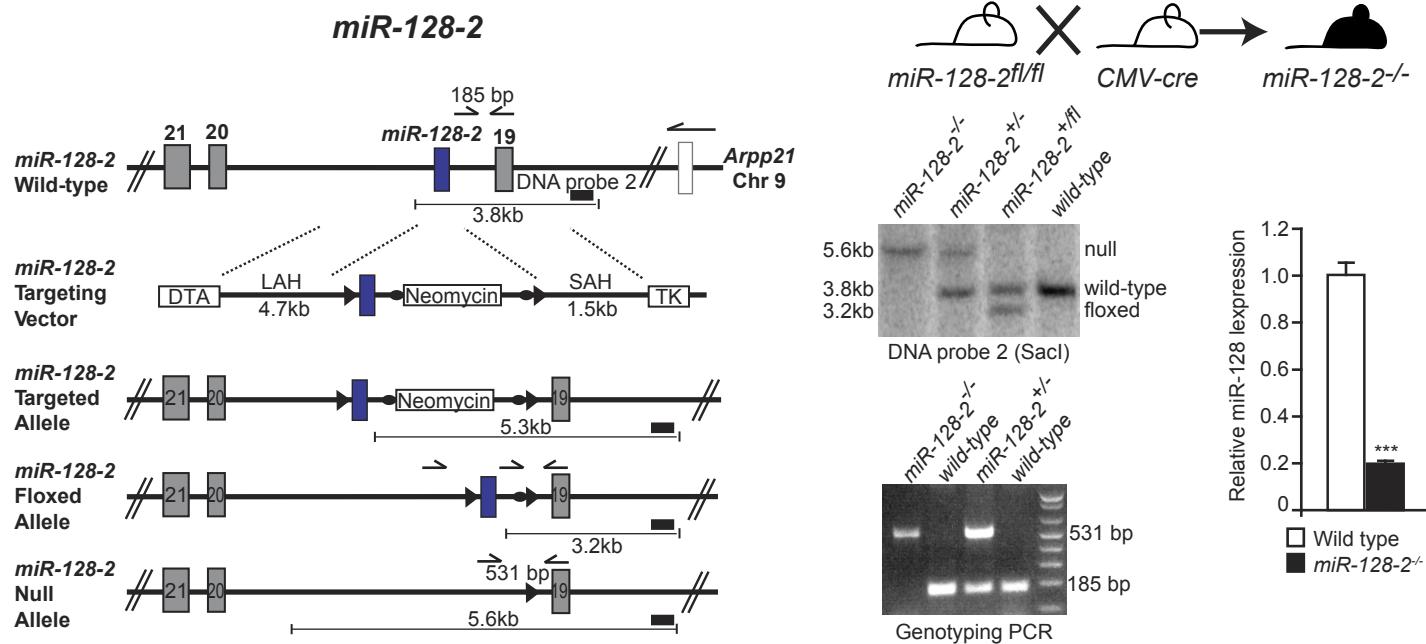
(A) miR-128 is enriched in the mouse brain. Expression levels of miR-128 were measured by qRT-PCR in RNA purified from the brain, skeletal muscle, heart, kidney, lung, and liver of 8-week old adult mice (n=3). The expression levels of miR-128 were normalized to snoRNA135 expression and displayed as fold increase over respective miRNA expression levels in the liver. 1-way ANOVA followed by Turkey's posttest, p<0.01 for brain vs. other organ comparisons. **(B) Postnatal brain development is accompanied by increase in miR-128 expression levels.** Expression levels of miR-128 and the neuron-enriched miR-124a were measured by qRT-PCR in the brain derived from mouse embryos at day 12 of embryonic development (E12), newborn mice (P0) or 8-week old adult mice (n=3 per age group). The expression levels of miRNAs were normalized to snoRNA135 expression and displayed as fold increase over respective miRNA expression levels in the E12 embryonic brain. **(C) miR-128 is expressed in different brain regions.** Expression of miR-128 in indicated brain regions in adult mice was quantified as in (A) and shown relative to mean miR-128 expression in the brain stem (n=3 per region). Error bars show s.e.m.

Figure S2.

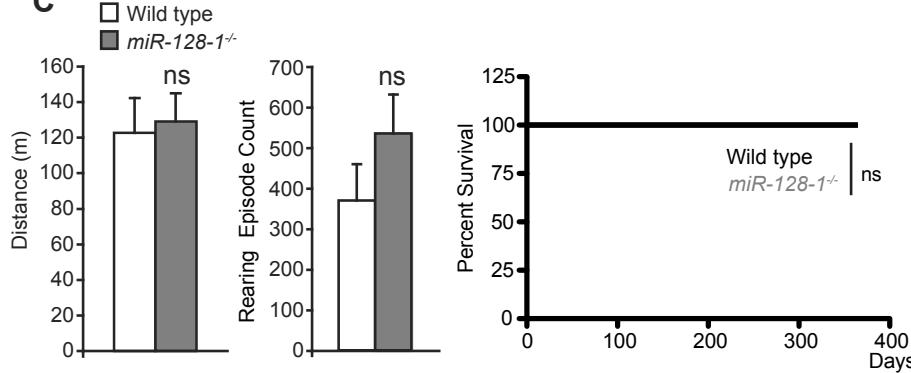
A



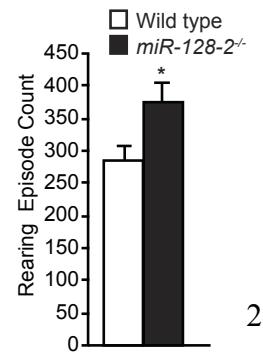
B



C



D



2

Figure S2. *miR-128-1* and *miR-128-2* genes contribute differentially to miR-128 expression in the brain.

(A, B) Generation of the (A) *miR-128-1* and (B) *miR-128-2* loci for conditional gene inactivation in mice. (Left panels) The strategy for gene modification and inactivation of *miR-128* genes are shown. The regions containing the miRNA hairpin in both of the miR-128 carrying genes were flanked with loxP sites in mouse ES cells followed by routine procedure for generation of *miR-128-1^{f/f}* and *miR-128-2^{f/f}* mice. MicroRNA hairpin, filled rectangle; exons, open rectangles; loxP sites, black triangles. Neomycin resistance gene flanked by FRT sequences (black circles) was removed from targeted loci by using FLT recombinase; DTA, diphtheria toxin gene; TK, thymidine kinase gene; LAH/SAH, long and short arm of homology. **(Right panels)** *miR-128-1* (*miR-128-1^{-/-}*) or *miR-128-2* (*miR-128-2^{-/-}*) deficient mice were generated by breeding *miR-128-1^{f/f}* and *miR-128-2^{f/f}* mice, respectively, to *CMV-cre* mice. Modified *miR-128-1* and *miR-128-2* alleles were identified by Southern blotting of the mouse tail DNA digested with EcoRI or SacI using the indicated DNA probes (black rectangles) or by PCR genotyping using primers as indicated in the scheme. The relative expression levels of miR-128 in the striatum of mice deficient for the *miR-128-1* (n=7 each) or *miR-128-2* (n=5 and 3) gene are shown. **(C) Inactivation of the *miR-128-1* gene does not affect motor activity or survival in mice.** The impact of *miR-128-1* deficiency on motor activity in mice was measured by using open field analysis. **(Left panel)** Total horizontal distance moved in meters and **(middle panel)** the number of vertical rearing episodes within 60 min in the open field are shown (n=7 and 9). **(Right panel)** The life spans of mice deficient for *miR-128-1* (n=6) and their respective wild-type littermate controls (n= 22) are shown. **(D) Inactivation of the *miR-128-2* gene increases exploration in mice.** The numbers of vertical rearing episodes of *miR-128-2^{-/-}* and littermate controls are shown (n=23 and 12).

Error bars show s.e.m., * p≤0.05, ** p≤0.01, Welch's t-test and log-rank test.

Figure S3

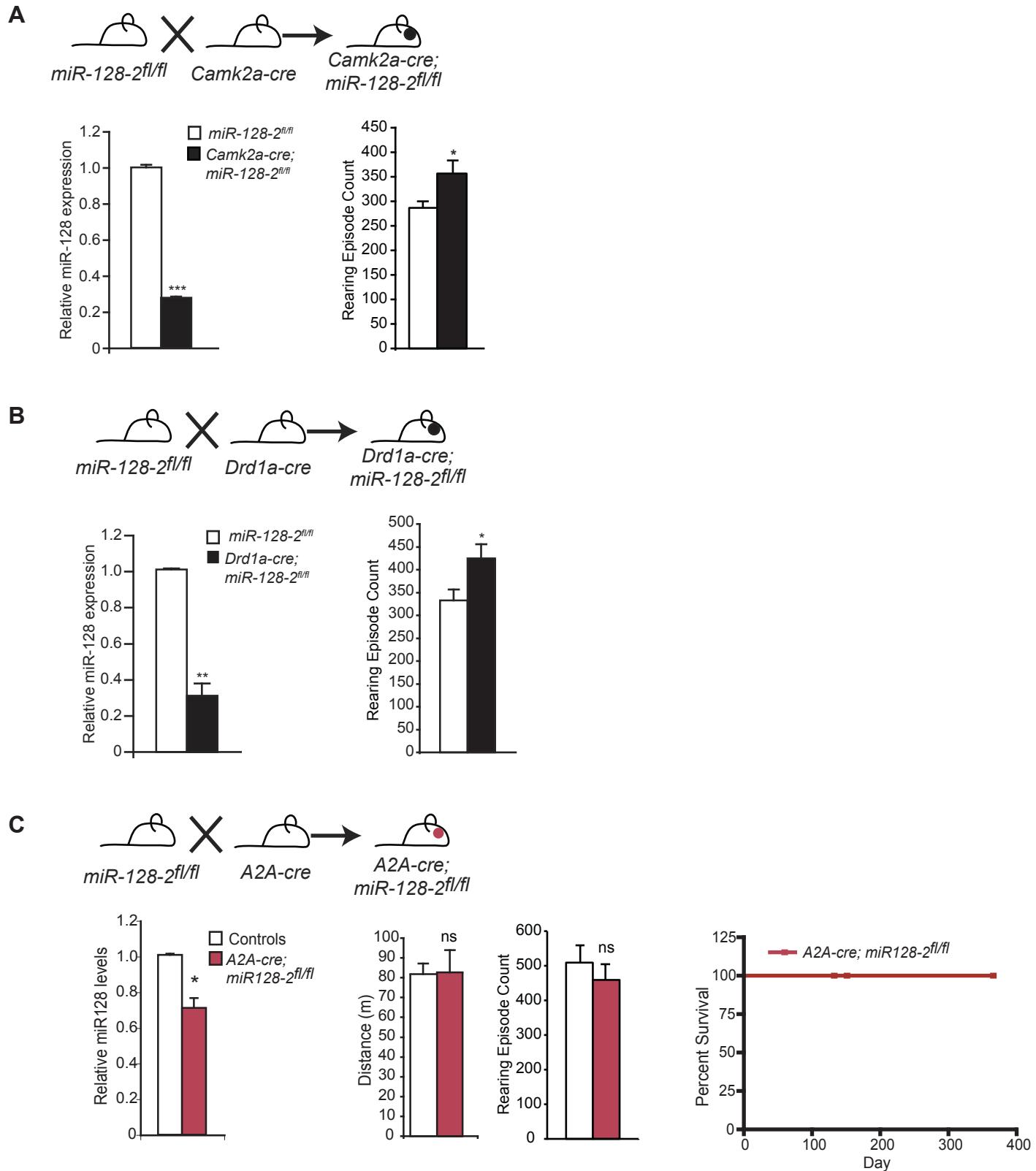


Figure S3. Increased explorative activity in mice with conditional inactivation in postnatal Camk2a- and D1-, but not D2-neurons in mice.

(A) miR-128 deficiency in postnatal Camk2a-neurons increases exploration.

miR-128 deficiency in postnatal Camk2a-neurons has been achieved by breeding *Camk2a-cre* with *miR-128-2^{f/f}* mice. **(Left panel)** The bar graph shows the relative miR-128 expression levels in *Camk2a-cre; miR-128-2^{f/f}* mice and control littermates (n=7 and 4). **(Right panel)** The number of vertical rearing episodes performed by *Camk2a-cre; miR-128-2^{f/f}* mice and control littermates (n=21 and 8) are shown.

(B) miR-128 deficiency in D1-neurons increases exploration. miR-128 deficiency in D1-neurons has been achieved by breeding *Drd1a-cre* with *miR-128-2^{f/f}* mice. Relative striatal miR-128 expression levels (left, n=3 each), and vertical rearing episodes (right) of *Drd1a-cre; miR-128-2^{f/f}* mice and control littermates (n=22 and 26) are shown. **(C) miR-128 deficiency in D2-neurons does not affect motor activity or survival in mice.** miR-128 deficiency in D2-neurons has been achieved by breeding *A2A-cre* with *miR-128-2^{f/f}* mice. Striatal miR-128 expression levels (left, n=3 each), horizontal motor activity and vertical rearing episodes (middle, n=9 and 7), and survival span (right, n= 8 and 7) of *A2A-cre; miR-128-2^{f/f}* mice and respective littermates (n=7) are shown.

Error bars show s.e.m., * p≤0.05, ** p≤0.01, Welch's t-test and log-rank test.

Figure S4

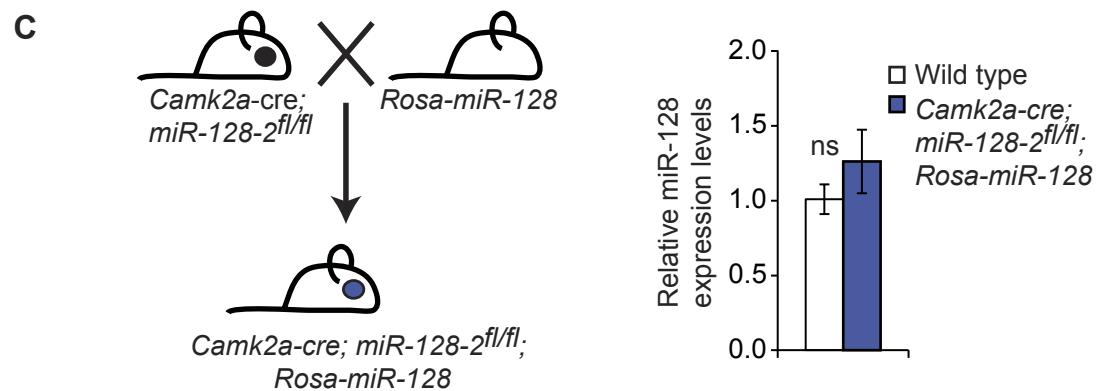
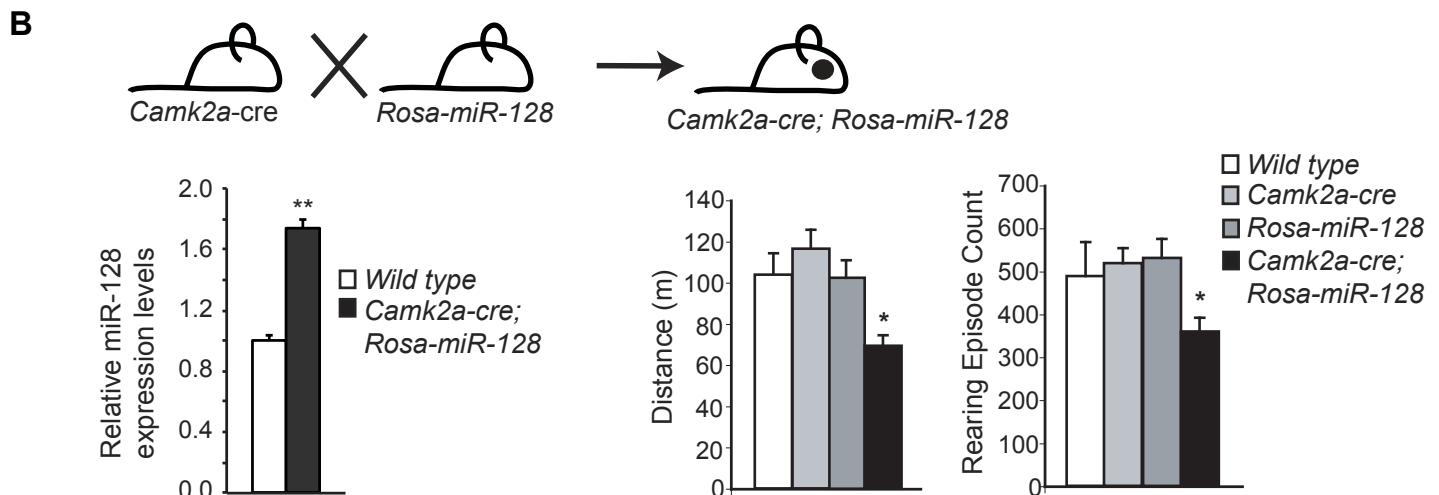
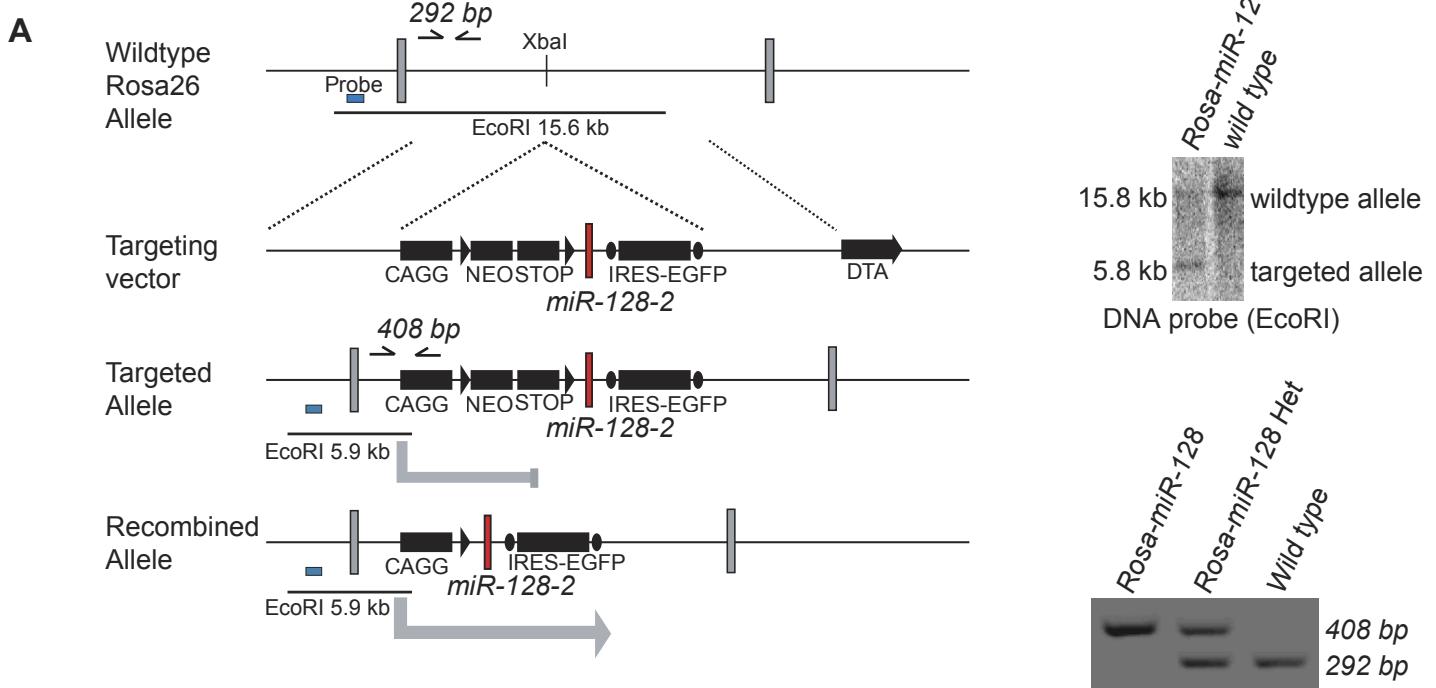


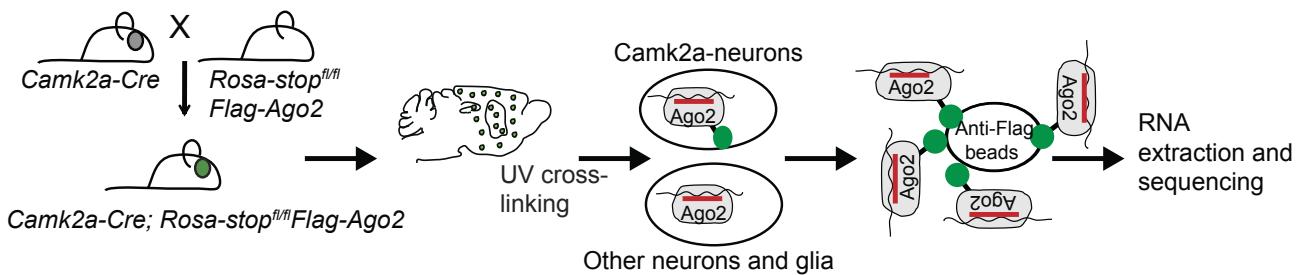
Figure S4. Ectopic expression of miR-128 *in vivo* attenuates motor activity in wild-type mice and normalizes miR-128 expression levels in *Camk2a-cre; miR-128-2^{f/f}* mice.

(A) Targeting strategy for the generation of mice with conditional overexpression of miR-128. The exogenous *miR-128-2* gene was inserted into the endogenous *Rosa26* gene locus in ES cells using a knock-in strategy as described previously (31). The *miR-128-2* gene (**red rectangle**) was separated from a strong CAGG promoter by a floxed-STOP-Neomycin cassette. Exons, grey rectangles. DTA, diphtheria toxin gene. The modified *ROSA-Stop^{f/f}-miR-128* allele (for simplification from now on called *Rosa-miR-128*) was confirmed by Southern blot analysis of the EcoRI digested DNA (**top right**) using the indicated DNA probe (**blue rectangle**) or by PCR genotyping (**bottom right**, primer locations as indicated in scheme). **(B) Reduced motor activity and exploration in mice with neuron-specific overexpression of miR-128.** **(Top)** Mice with postnatal neuron specific overexpression of miR-128 (*Camk2a-cre; Rosa-miR-128*) were generated by breeding *Camk2a-cre* with *Rosa-miR-128* mice. **(Left)** miR-128 expression levels in the striatum were measured by qRT-PCR (n=3 each) as described (Fig. S1) and are shown relative to mean miR-128 expression in the wild type striatum. Welch's t-test. **(Middle and right)** Total horizontal distance and rearing activity in an open-field over 60 minutes for *Camk2a-cre; Rosa-miR-128* mice (n=21) and littermate controls (wild type n=8, *Camk2a-cre* n=5, *Rosa-miR-128* n=17) are shown. 1-way ANOVA followed by Turkey's post test. **(C) Ectopic expression of miR-128 from the Rosa26 locus normalizes miR-128 expression levels in *Camk2a-cre; miR-128-2^{f/f}* mice.** **(Left)** Mice with postnatal neuron specific knock-out of *miR-128-2* and ectopic expression of *miR-128-2* from the *Rosa26* locus (*Camk2a-cre; miR-128-2^{f/f}; Rosa-miR-128*) were generated by breeding *Camk2a-cre; miR-128-2^{f/f}* to *Rosa-miR-128* mice. **(Right)** miR-128 expression in the striatum of *Camk2a-cre; miR-128-2^{f/f}; Rosa-miR-128* mice (n=4) was measured by qRT-PCR and data are shown relative to mean expression in littermate controls (n=3). Welch's t-test.

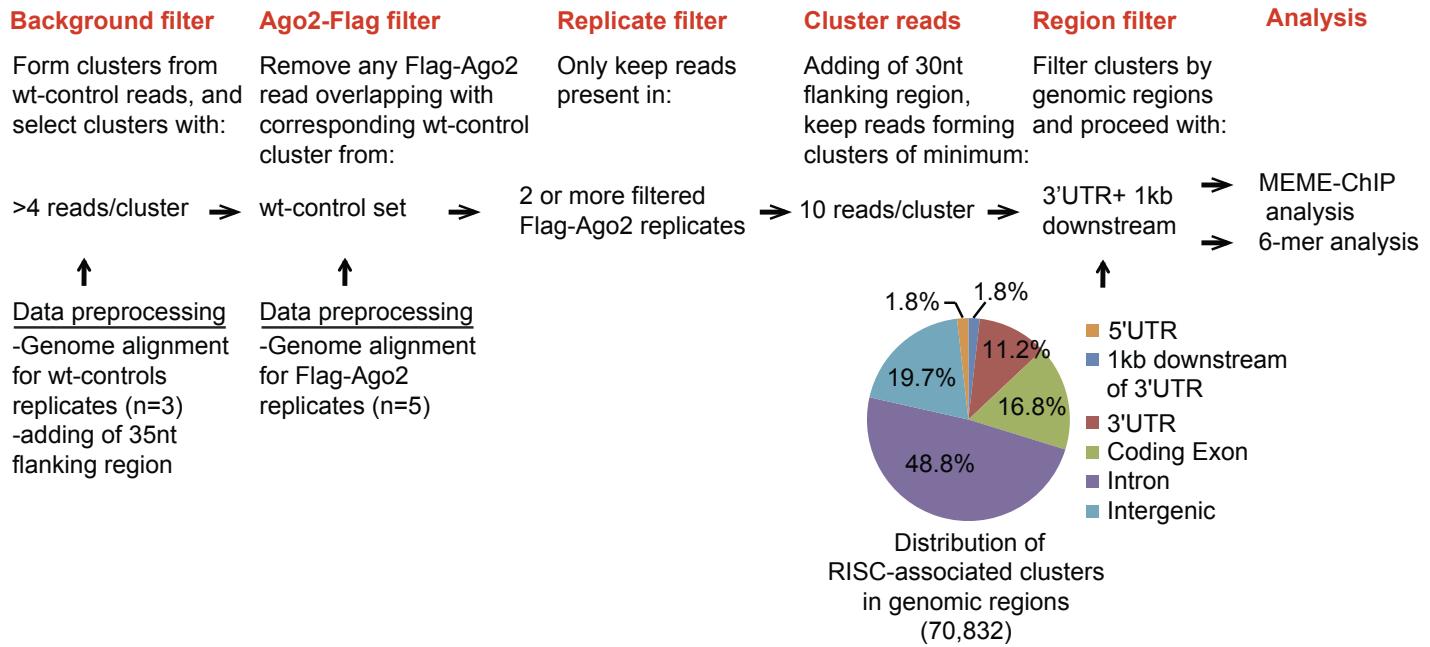
Error bars show s.e.m., * p≤0.05, ** p≤0.01.

Figure S5

A



B



C

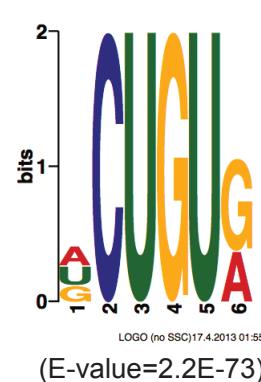
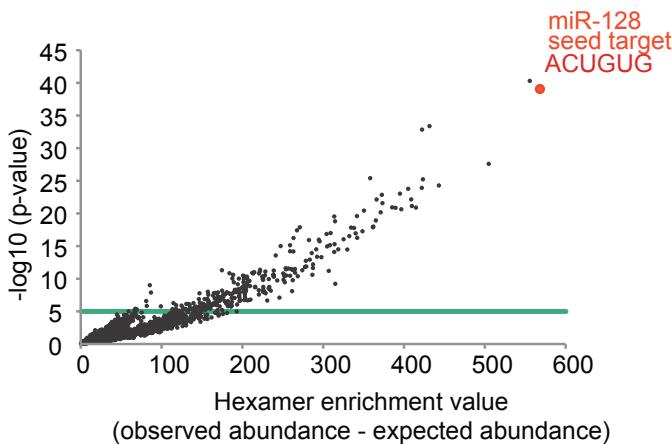
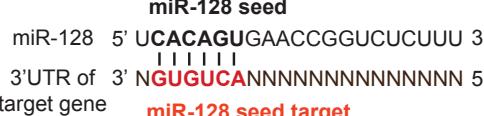
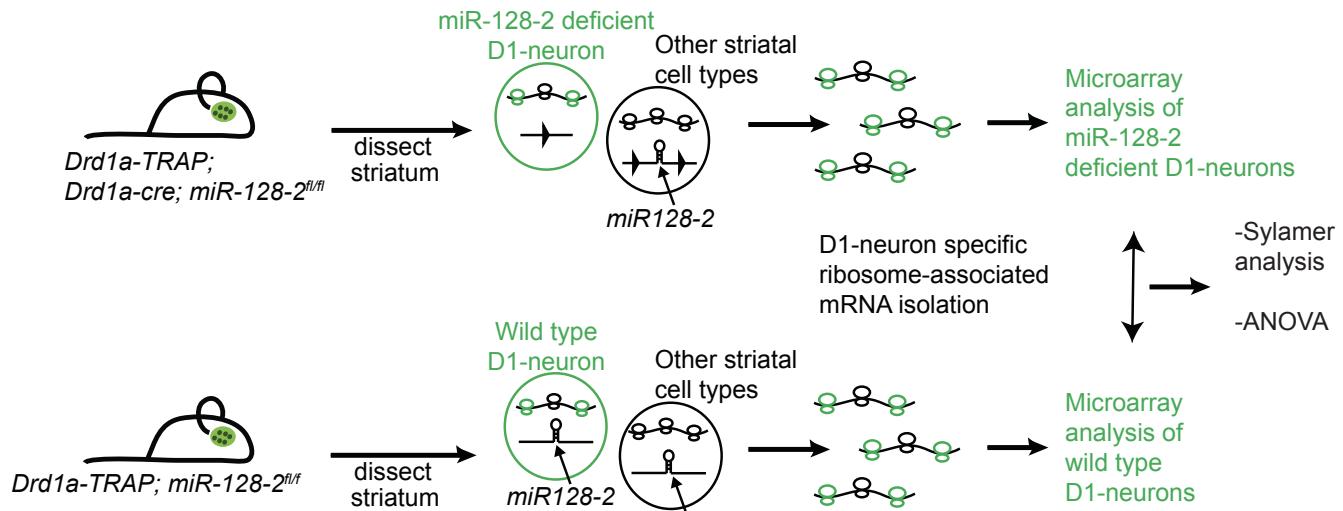


Figure S5. Strategy of neuron specific RISC-associated mRNA isolation and analysis.

(A) Identification of RISC-associated RNAs in Camk2a-neurons in mice. The scheme outlines the experimental procedure for the isolation of Camk2a-neuron specific RISC-associated mRNAs from adult mice. The Cre-mediated expression of Flag-tagged Ago2 in Camk2a-neurons was achieved by breeding *Camk2a-cre* mice to *Rosa-Stop^{fl/fl}-Flag-Ago2* mice (8). The Flag-tagged Ago2 (green) was immunoprecipitated from lysates of Camk2a-neurons followed by isolation and sequencing of the RISC-associated RNAs as described in Material and Methods. **(B) Schematic overview for computational analysis of HITS-CLIP data from RISC-associated RNAs in neurons.** The flowchart displays the subsequent steps of data analysis as detailed in Supplementary Material and Methods. The Venn diagram displays the genomic distribution (Mouse Genome Reference Consortium, version mm10) of RISC-associated RNA clusters (70,832). **(C) Putative miR-128 targets are highly enriched among RISC-associated mRNAs in neurons.** **(Upper panel)** Scheme shows the miR-128 seed sequence (**bold black**) and the corresponding target seed sequence (**bold red**) within the 3'UTR of a potential miR-128 target gene. **(Lower panel, left)** Putative miR-128 targets are highly enriched among RISC-associated mRNAs in Camk2a-neurons. Scatter plot displays relative enrichment of all possible nucleotide hexamer sequences (4096) within the 3'UTR + 1 kb downstream sequence of RISC-associated mRNA clusters (8794). The hexamer alignment with the RefSeq annotated 3'UTR+1kb shows the highest degree of enrichment for the miR-128 seed target sequence (**red dot**). X-axis shows the observed frequency of a hexamer that exceeds the normalized frequency of occurrences in the corresponding RefSeq region, y-axis shows $-\log_{10}$ (p-value) from chi-squared test, green line represents Bonferroni-corrected critical p-value: $0.05/(4^6) = 1.22 \times 10^{-5}$. **(Middle)** Motif analysis of RISC-associated 3'UTR +1kb mRNAs clusters using MEME-Chip software identifies the miR-128 seed target sequence as the second highest enriched motif (E-value=2.2E-73).

Figure S6

A



B

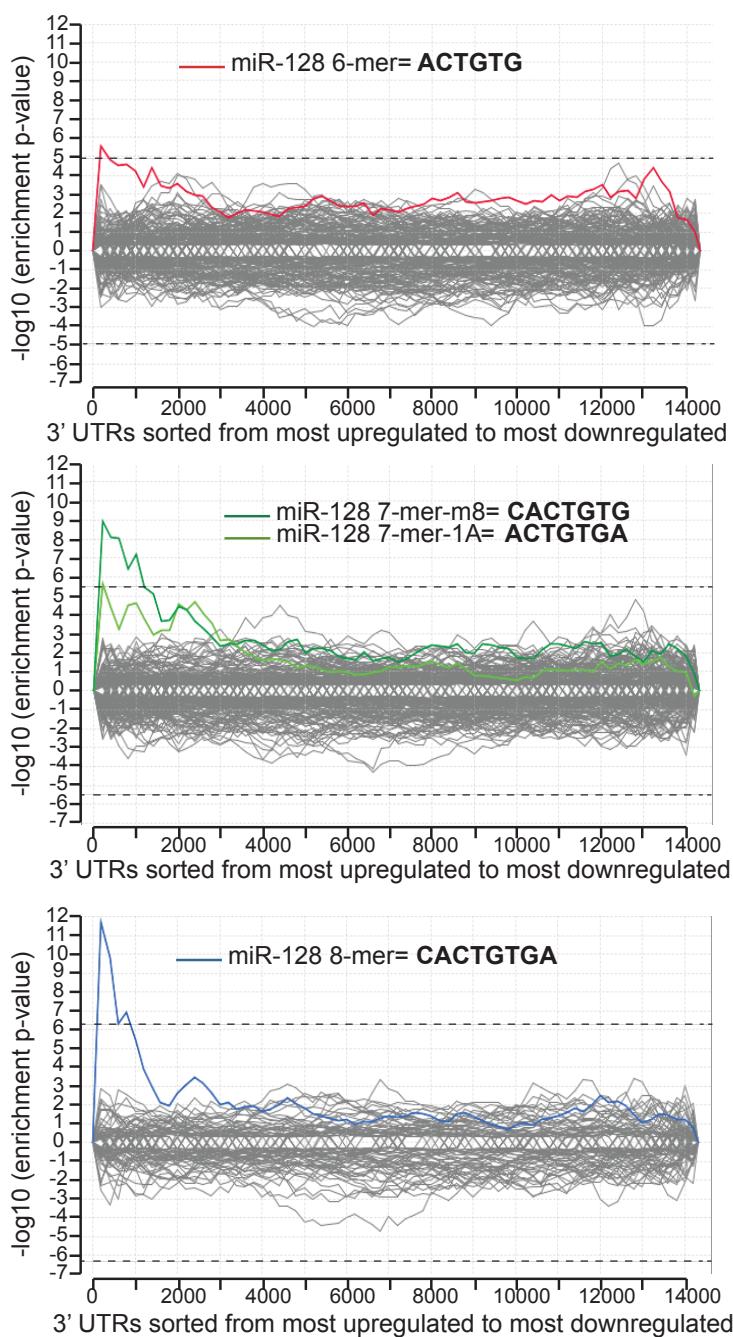
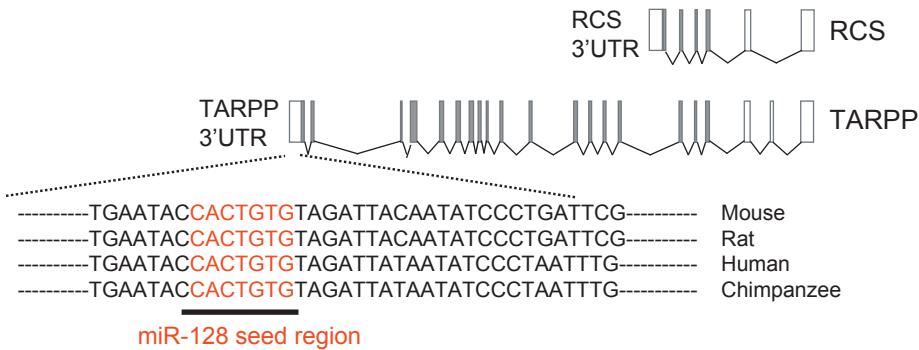


Figure S6. Identification of primary miR-128 target genes in D1-neurons.

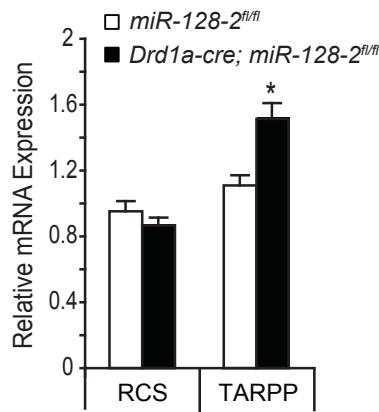
(A) The neuron-specific profiling of polyribosome-associated mRNAs in wild type and miR-128 deficient D1-neurons. Polyribosome-associated mRNA transcripts were isolated from the striatum of control *Drd1a-TRAP*; *miR-128-2^{f/f}* or mutant *Drd1a-TRAP*; *Drd1a-cre*; *miR-128-2^{f/f}* mice (n=5/genotype) that express the eGFP-L10 protein in D1-neurons. The analysis of polyribosome-associated mRNAs has been performed as detailed in Supplementary Material and Methods. Differentially expressed genes between wild type and miR-128 deficient D1-neurons were identified by ANOVA. Green circles: D1-neurons; black circles: other cell types; green ribosomes: eGFP-tagged ribosome; black ribosomes: untagged ribosomes. **(B) 3'UTR's containing the miR-128 seed target sequence are significantly enriched among genes that are most up-regulated in miR-128 deficient D1-neurons.** Dataset from the D1-neuron TRAP experiments were analyzed using Sylamer algorithm to determine if potential miR-128 target genes were more abundant among 3'UTR's of mRNAs most upregulated in miR-128 deficient D1-neurons as compared to the rest. Sylamer enrichment landscapes show results for 6-nucleotide (top), 7-nucleotide (middle) and 8-nucleotide (bottom) sequences. The x-axes represent 3'UTRs ranked from the most upregulated (left) to the most downregulated (right) gene in miR-128 deficient D1-neurons. The y-axes show hypergeometric significance for each sequence at each leading bin (-log10 (P-value)). Horizontal dotted lines indicate Bonferroni-corrected p-value threshold of 0.05. The 4 colored lines indicate the sequences complementary to miR-128 seed. Among all tested 6-, 7- and 8-nucleotide sequences, only these four miR-128 seed target sequences show peak enrichment with p-values ≤ 0.05 .

Figure S7

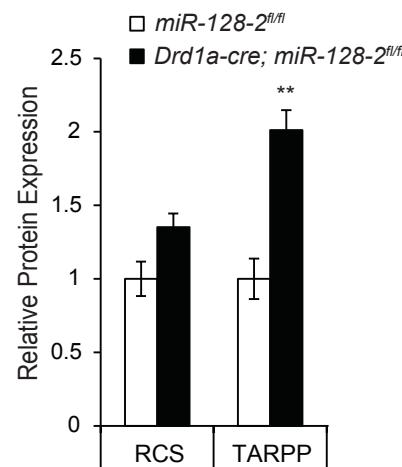
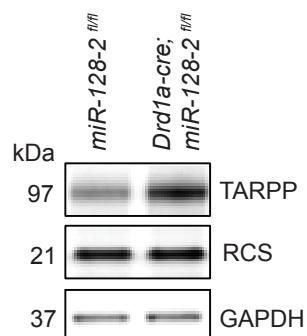
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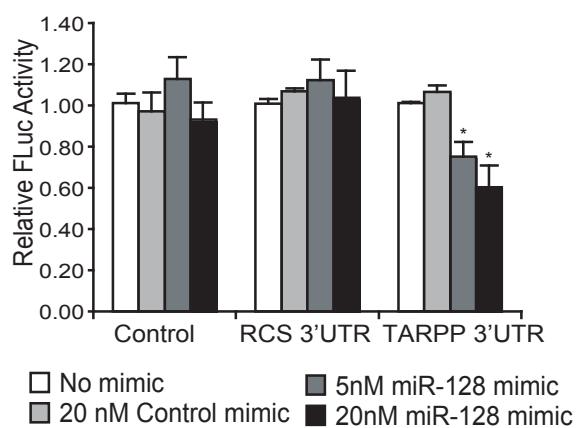
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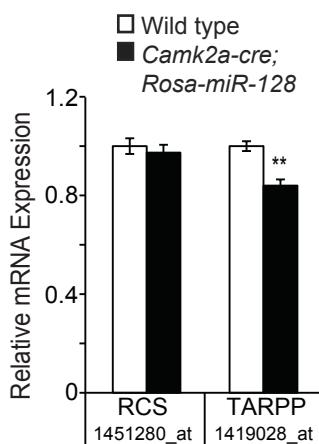


Figure S7. miR-128 suppresses the expression of the TARPP-encoding long splice variant of the miR-128-2 host gene *Arpp21*.

(A) The TARPP-encoding mRNA splice variant of the *Arpp21* gene contains a miR-128 target seed sequence in the 3'UTR. The scheme illustrates the two transcript isoforms of the *Arpp21* gene that encode the TARPP and RCS proteins. The 3'UTR of the long isoform TARPP contains a highly conserved miR-128 target seed sequence (shown in red). **(B, C) miR-128 deficiency leads to de-repression of TARPP.** **(B)** qRT-PCR quantification of RNA prepared from the striatum of *Drd1a-cre; miR-128-2^{f/f}* mice and their littermate controls (n=3 each) show that only the long TARPP-encoding mRNA is upregulated in the absence of miR-128. **(C)** Expression levels of RCS (21 kDa) and TARPP (97 kDa) proteins in protein lysates from *Drd1a-cre; miR-128-2^{f/f}* or littermate controls (n=3 each) were analyzed by Western blot. Bar graphs summarizes the mean protein expression levels as normalized to GAPDH. **(D, E) Specific suppression of TARPP in neurons overexpressing miR-128.** **(D)** The ability of miR-128 to target the 3'UTR of the TARPP and RCS mRNAs was analyzed using an *in-vitro* luciferase reporter assay. Plasmids expressing the firefly luciferase upstream of the RCS and TARPP specific 3'UTR sequence were transfected into N2A cells in the absence or presence of miR-128 mimics at the indicated concentrations. Firefly Luciferase activity was normalized to reporter Renilla Luciferase activity and visualized as activity relative to control transfections with no mimics added (n=3). **(E)** The level of mRNA expression of TARPP and RCS in the striatum of mice with a postnatal neuron specific overexpression of miR-128 and their littermate controls (n=4 each) were analyzed using Affymetrix microarray analysis. Mean normalized expression values corresponding to probes that are specific for the RCS and TARPP splice variant are shown. Error bars show sem. * p≤0.05, ** p≤0.01, *** p≤0.001, p-values calculated by Welch's t-test.

Figure S8

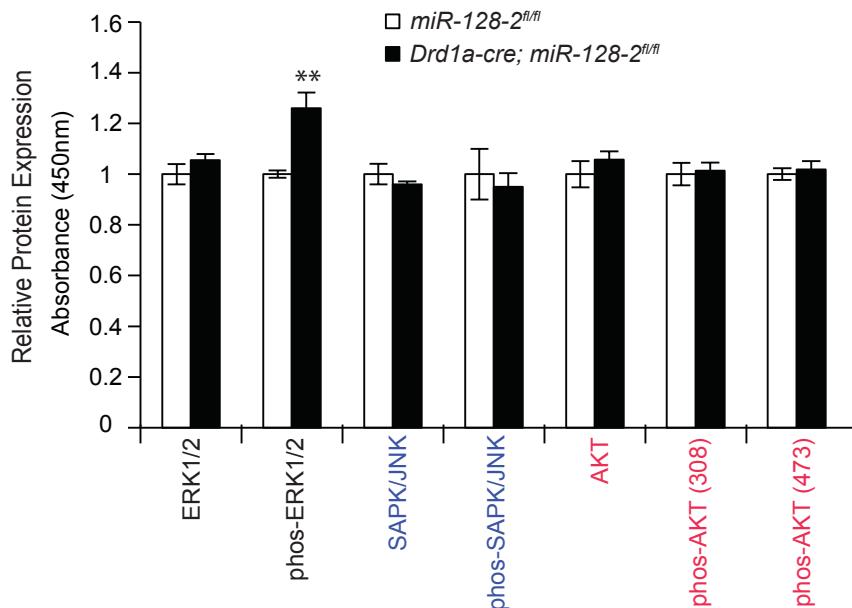
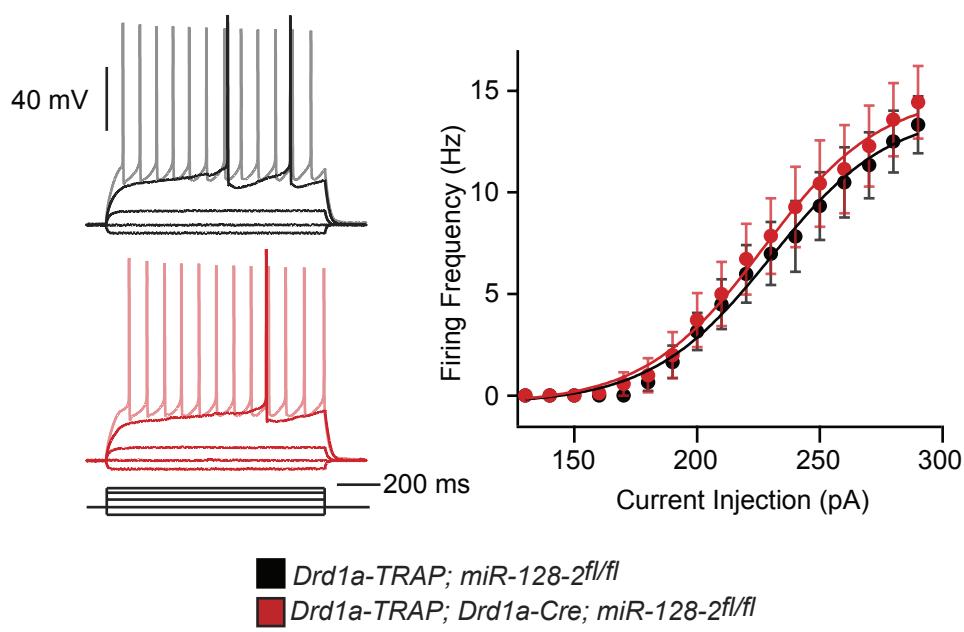


Figure S8. Deficiency of miR-128 in D1-neurons leads to increase in ERK2 phosphorylation.

Relative quantity of total or phosphorylated MAP kinase pathway proteins ERK1/2, SAPK/JNK, and AKT in striatal lysates from *Drd1a-cre; miR-128-2^{fl/fl}* and littermate controls (n=4) were quantified by ELISA. Relative protein expression levels are based on absorbance values (450 nm) and displayed as bar graphs normalized to control values. Error bars show sem. ** p≤0.01, p-values calculated by Welch's t-test.

Figure S9

A



B

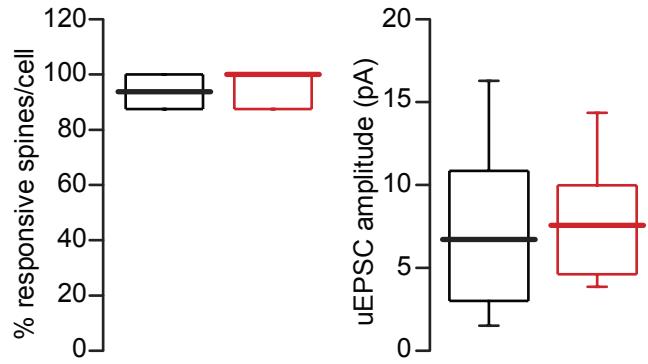
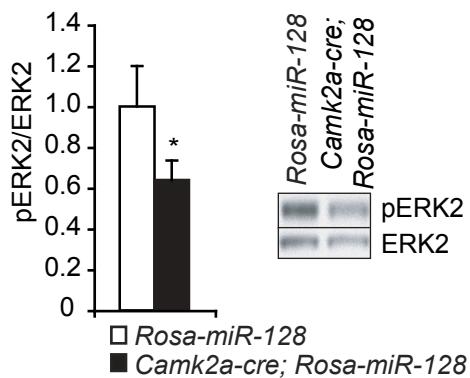


Figure S9. miR-128 deficient striatal D1-neurons display D1-neuron characteristic somatic excitability.

(A, left) Representative D1-neuron prototypic responses of control (*Drd1a-TRAP; miR-128-2^{f/f}*, **top, black**) and miR-128 deficient (*Drd1a-TRAP, Drd1a-cre; miR-128^{f/f}*, **bottom, red**) D1-neurons to somatic current injections. D1-neurons were identified by eGFP-L10 expression, voltage traces are in response to -100, -50, +100, +190 and +250 pA. **(A, right)** Frequency-current (F-I) plot showing D1-neuron characteristic average firing frequencies to somatic current injection. No difference was observed between wild-type (**black**, n=6) and mutant (**red**, n=7) D1-neurons. Mann-Whitney nonparametric test, p>0.05. **(B) miR-128 controls the number of functional spines in D1-neurons.** 2 photon uncaging of glutamate on successive neighboring spine heads revealed similar success rates for producing somatic EPSCs in control and miR-128 deficient D1 neurons (**n=5-6 cells, 40-48 spines per group, left**), suggesting the increased spine density in (**Fig. 3B**) represents an increase in the number of spines with functional glutamate receptors. Glutamate uncaging-induced somatic EPSC amplitudes were similar in both groups (**right**).

Figure S10

A



B

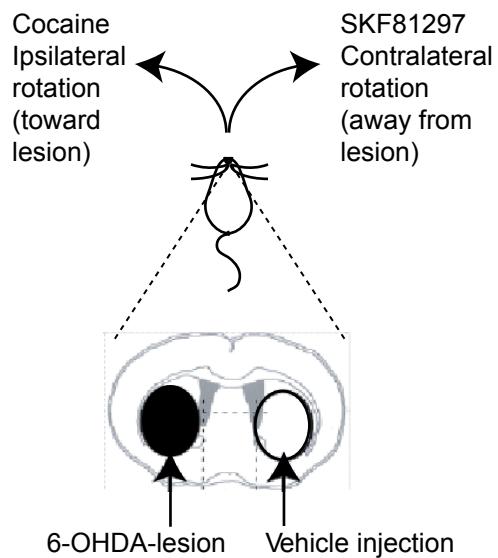


Figure S10. Increased miR-128 expression in neurons suppresses ERK2 activation and protects against abnormal motor activity and seizures associated with chemically induced Parkinson's disease and seizures.

(A) miR-128 overexpression in Camk2a-neurons suppresses ERK2 phosphorylation in mice. ERK2 phosphorylation levels in the striatum of transgenic *Camk2a-cre; Rosa-miR-128* mutant and control mice (n=4 each) were quantified by Western blotting, normalized to total ERK2 expression, and displayed relative to mean control levels. Representative blot is shown. Welch's t-test, * p≤0.05. **(B) miR-128 overexpression attenuates chemically triggered hyperresponsive motor behavior in mice.** The scheme shows the standard rotational responses of wild type mice with unilateral 6-OHDA-induced lesion. 6-OHDA and vehicle were injected into the left and right striatum, respectively, and rotational responses to either cocaine (which inhibits endogenous dopamine reuptake at dopaminergic terminals and thereby increases synaptic dopamine levels) or the Drd1-agonist SKF81297 (specific activation of the dopamine D1 receptor (Drd1)) are assayed after a 3-week recovery period. Cocaine injections induce ipsilateral (towards the lesioned side) rotations due to the stronger activation of the unlesioned contralateral striatum that still contains the functional dopaminergic terminals. Injections of the Drd1-agonist SKF81297 induce contralateral rotations (away from the lesioned side) due to the abnormal hypersensitivity of D1-neurons to Drd1 activation after dopamine depletion in the lesioned, ipsilateral striatum.

Table S1.

Overrepresented hexamers in RISC-associated 3'UTR clusters obtained from adult Camk2a-neurons.

Table S2.

Putative miR-128 RISC-associated target genes in adult Camk2a-neurons.

Table S3.

154 unique RISC-associated miR-128 target genes (189 microarray probes) that showed significantly ($p \leq 0.05$) increased ribosome-association in miR-128 deficient D1-neurons.

Table S4.

miR-128 targets in D1-neurons are enriched in ion channels, ion transporters, and signaling proteins.

Movie S1. Tonic clonic seizure preceding miR-128-2^{-/-} mouse death.

Fatal tonic clonic seizure of a miR-128-2^{-/-} mouse in Camera 1 (**Top Left**).

Table S1. Overrepresented hexamers in RISC-associated 3'UTR clusters obtained from adult Camk2a-neurons.

6mer sequence	# times in Ago2-CLIP cluster	# times in RefSeq background	Enrichment (observed-expected)	P-value	-log10(P-value)	z-score
ACTGTG	1211	643	568	1.04E-39	38.98	6.02
GGGCTG	1136	581	555	5.94E-41	40.23	5.89
CTGTGG	1300	796	504	3.03E-28	27.52	5.35
CTGTGA	1143	700	443	6.16E-25	24.21	4.69
GACTGT	844	413	431	5.04E-34	33.30	4.57
GAGGAG	1020	597	423	7.00E-26	25.16	4.48
GGACTG	823	401	422	1.71E-33	32.77	4.47
TGTGGG	1060	638	422	1.44E-24	23.84	4.47
GCTGTG	1152	738	414	1.52E-21	20.82	4.39
GGGAGG	1115	706	409	8.53E-22	21.07	4.34
GGAGGG	1068	660	408	8.42E-23	22.07	4.33
TGTGGA	990	585	405	2.01E-24	23.70	4.29
GGAAGG	1073	677	396	2.73E-21	20.56	4.20
GGAGGA	971	576	395	1.11E-23	22.95	4.18
AGGAGG	1029	640	389	1.64E-21	20.79	4.13
GGCTGG	1006	621	385	1.40E-21	20.85	4.08
GAGAGG	926	553	373	3.12E-22	21.51	3.95
GAGGGG	880	508	372	1.68E-23	22.78	3.95
GGGCAG	970	599	371	8.04E-21	20.09	3.93
AGACTG	875	509	366	8.60E-23	22.07	3.88
GGAGAG	994	629	365	1.39E-19	18.86	3.87
GGAAGA	1023	661	362	1.22E-18	17.91	3.83
TGGGGA	1025	664	361	1.55E-18	17.81	3.83
GGTGCT	753	395	358	4.70E-26	25.33	3.79
GAAGGG	865	515	350	4.38E-21	20.36	3.71
GAGAGA	989	641	348	6.38E-18	17.20	3.69
GGGAAG	1007	665	342	6.51E-17	16.19	3.62
GGCTGT	856	515	341	2.99E-20	19.52	3.62
GAGAAC	961	621	340	1.32E-17	16.88	3.60
GGGGAG	913	575	338	2.00E-18	17.70	3.58
GGACAG	892	558	334	1.73E-18	17.76	3.54
GAAGAG	941	609	332	3.48E-17	16.46	3.52
AGAGAG	1044	715	329	3.99E-15	14.40	3.49
GTGGGG	929	604	325	1.08E-16	15.97	3.44
GCTGGG	978	660	318	3.72E-15	14.43	3.37
TGTGTG	1460	1145	315	7.11E-10	9.15	3.33
CTGTAG	764	450	314	1.88E-19	18.72	3.33
GGCAGG	909	595	314	6.08E-16	15.22	3.33
TGTAGA	736	423	313	3.49E-20	19.46	3.32
GCAGAG	974	661	313	9.37E-15	14.03	3.32
AGGGCT	806	497	309	1.19E-17	16.93	3.27
GTGTGG	886	578	308	8.42E-16	15.07	3.26
AGGAAG	1155	849	306	7.50E-12	11.13	3.25
GTGCTG	878	574	304	1.33E-15	14.87	3.23
AGGGGA	788	484	304	1.67E-17	16.78	3.22
AGAGGA	933	636	297	5.93E-14	13.23	3.15
GTGGGA	794	499	295	2.21E-16	15.66	3.13
GTGGAG	779	485	294	1.26E-16	15.90	3.12
GAGCTG	898	606	292	5.08E-14	13.29	3.10

AGAGGG	830	539	291	3.73E-15	14.43	3.08
TGGAGA	945	658	287	7.56E-13	12.12	3.04
CTGGAG	985	698	287	2.69E-12	11.57	3.04
TGCTGT	1070	784	286	2.97E-11	10.53	3.03
GGGAGA	830	545	285	1.39E-14	13.86	3.03
GAAGGA	874	591	283	1.41E-13	12.85	3.00
GGGGCT	723	441	282	1.42E-16	15.85	2.99
AGGGAG	917	638	279	1.59E-12	11.80	2.95
TGGAGG	857	579	278	2.15E-13	12.67	2.95
TGGGAG	911	634	277	1.81E-12	11.74	2.94
AGGAGA	928	654	274	5.93E-12	11.23	2.90
GGGGAC	610	339	271	1.57E-18	17.81	2.87
CTGGGG	966	698	268	4.92E-11	10.31	2.84
TGGTGC	609	342	267	4.60E-18	17.34	2.83
CACTGT	901	636	265	1.43E-11	10.84	2.81
GAGCAG	859	594	265	3.84E-12	11.42	2.81
GGGACT	627	364	263	6.83E-17	16.17	2.79
ACTGTA	703	440	263	7.89E-15	14.10	2.78
TGGGGG	855	593	262	5.64E-12	11.25	2.78
CTGGGA	979	717	262	2.02E-10	9.70	2.78
CTGCTG	1165	904	261	9.43E-09	8.03	2.77
GGAGAA	834	574	260	3.94E-12	11.40	2.76
GGTGGG	898	639	259	4.16E-11	10.38	2.74
GAACTG	682	423	259	7.28E-15	14.14	2.74
GAATGG	646	387	259	8.78E-16	15.06	2.74
TTGGGG	806	549	257	3.22E-12	11.49	2.72
AGAAGG	864	610	254	3.82E-11	10.42	2.69
GAGGGA	797	543	254	4.21E-12	11.38	2.69
GGCAGA	784	531	253	2.94E-12	11.53	2.68
TGGCTG	940	688	252	4.17E-10	9.38	2.67
GAGGAA	850	599	251	4.03E-11	10.39	2.66
GGAAAG	894	644	250	1.68E-10	9.78	2.66
TGTGAG	818	568	250	1.82E-11	10.74	2.65
AAGGGC	599	352	247	1.18E-15	14.93	2.62
CTGTGT	1180	935	245	9.41E-08	7.03	2.60
GGGTGG	853	610	243	2.21E-10	9.66	2.57
GAATGA	624	383	241	3.20E-14	13.50	2.55
TGGGCT	782	544	238	5.80E-11	10.24	2.53
AGAGAC	722	484	238	6.58E-12	11.18	2.53
TGAGAG	765	527	238	3.41E-11	10.47	2.53
TGTGGC	758	520	238	2.99E-11	10.52	2.52
AGGCAG	945	710	235	7.93E-09	8.10	2.49
TGGAAG	873	640	233	2.14E-09	8.67	2.47
GCAGGG	770	538	232	1.35E-10	9.87	2.46
CTGAGA	890	658	232	3.64E-09	8.44	2.46
TCTGTG	1114	884	230	2.57E-07	6.59	2.44
AGAAGA	943	715	228	2.01E-08	7.70	2.42
GTGGTG	674	446	228	9.49E-12	11.02	2.42
GCTGGA	705	478	227	3.71E-11	10.43	2.41
AGGCTG	895	669	226	1.07E-08	7.97	2.40
TGTGAA	861	636	225	5.59E-09	8.25	2.39
CAGGAG	899	674	225	1.30E-08	7.89	2.39
CTGGGC	822	597	225	2.14E-09	8.67	2.39
TGACTG	736	511	225	1.80E-10	9.74	2.39

GCAGGA	724	499	225	1.28E-10	9.89	2.38
TTGTGG	697	473	224	5.54E-11	10.26	2.38
GAGACT	625	404	221	5.05E-12	11.30	2.35
GGGGGA	635	414	221	8.18E-12	11.09	2.35
GTGGAA	647	427	220	1.83E-11	10.74	2.33
GCTGCT	900	680	220	3.10E-08	7.51	2.33
AGCTGG	830	610	220	6.81E-09	8.17	2.33
TGAGGA	760	544	216	2.41E-09	8.62	2.28
TGGTGG	753	538	215	2.09E-09	8.68	2.28
TGGACT	606	392	214	1.18E-11	10.93	2.27
GGAGAC	608	395	213	1.81E-11	10.74	2.26
TGGGAC	599	387	212	1.53E-11	10.82	2.25
CAGAGG	914	704	210	1.88E-07	6.73	2.22
GGCTGC	704	495	209	1.57E-09	8.80	2.22
GGAGGC	647	439	208	2.56E-10	9.59	2.21
GGATGG	636	429	207	2.31E-10	9.64	2.19
TGGGAA	901	695	206	2.44E-07	6.61	2.19
AGGACT	646	440	206	4.45E-10	9.35	2.18
AGGGGC	594	389	205	5.82E-11	10.24	2.18
TGTTGG	677	472	205	1.43E-09	8.85	2.17
CTGGAC	600	396	204	9.55E-11	10.02	2.17
GGGGTG	712	508	204	5.11E-09	8.29	2.16
AAGGGA	736	532	204	1.05E-08	7.98	2.16
TGCTGC	819	616	203	8.61E-08	7.06	2.15
GGGGCA	580	377	203	5.70E-11	10.24	2.15
GAAAGG	769	566	203	2.93E-08	7.53	2.15
GGGGAA	696	494	202	4.32E-09	8.36	2.15
CTGAGG	863	661	202	2.22E-07	6.65	2.14
GGAGTG	590	389	201	1.20E-10	9.92	2.14
TGGGCG	656	455	201	1.60E-09	8.80	2.13
TGAAGG	719	518	201	1.11E-08	7.96	2.13
GAGTGG	616	415	201	3.93E-10	9.41	2.13
GAGGAC	560	360	200	3.89E-11	10.41	2.12
GGGACA	660	461	199	2.80E-09	8.55	2.11
CAGGGA	828	631	197	2.40E-07	6.62	2.09
AAGAGG	699	502	197	1.42E-08	7.85	2.08
CTGTGC	827	631	196	2.82E-07	6.55	2.08
TGGCAG	764	568	196	8.12E-08	7.09	2.08
CTGGTG	737	541	196	4.37E-08	7.36	2.08
AGGGGG	556	361	195	1.14E-10	9.94	2.07
GTGCCT	651	456	195	4.65E-09	8.33	2.07
AAGGGG	596	402	194	8.32E-10	9.08	2.06
TGCCTT	878	685	193	1.04E-06	5.98	2.05
GTGTGT	1066	873	193	1.23E-05	4.91	2.04
TGAGGG	668	476	192	1.34E-08	7.87	2.04
GGAGCT	633	442	191	5.64E-09	8.25	2.03
TGGATG	633	443	190	6.78E-09	8.17	2.02
GGCCTG	734	544	190	1.05E-07	6.98	2.02
GTTGGG	552	363	189	4.19E-10	9.38	2.00
GTAGAG	495	307	188	2.99E-11	10.52	2.00
GCACTG	652	464	188	1.83E-08	7.74	1.99
TGTAGG	514	327	187	1.09E-10	9.96	1.98
GCTGAG	775	588	187	4.25E-07	6.37	1.98
GTGGCT	707	521	186	1.05E-07	6.98	1.98

TGCTGG	837	651	186	1.39E-06	5.86	1.97
GGCAGC	657	471	186	3.06E-08	7.51	1.97
AAGAGA	848	662	186	1.77E-06	5.75	1.97
GAAGAA	858	672	186	2.10E-06	5.68	1.97
GCCTGG	814	630	184	1.26E-06	5.90	1.95
GTGGAC	464	280	184	1.71E-11	10.77	1.95
GAGGTG	627	444	183	2.09E-08	7.68	1.94
AGCAGA	819	637	182	1.91E-06	5.72	1.93
CTGTTG	722	540	182	3.14E-07	6.50	1.93
AGAGAA	993	812	181	2.14E-05	4.67	1.91
AGGGAC	595	415	180	1.38E-08	7.86	1.91
CTGAGC	754	574	180	7.91E-07	6.10	1.91
GGAGCA	605	426	179	2.45E-08	7.61	1.90
TGGGTG	724	545	179	5.02E-07	6.30	1.90
ACTGAG	695	517	178	3.26E-07	6.49	1.89
GTGAGG	619	443	176	6.29E-08	7.20	1.87
GATGGA	592	416	176	3.00E-08	7.52	1.87
CCTGTG	973	797	176	3.02E-05	4.52	1.86
TCTGGG	847	672	175	7.45E-06	5.13	1.85
TGGACA	629	455	174	1.15E-07	6.94	1.85
GGTGGA	544	370	174	7.85E-09	8.11	1.85
GGATTG	408	234	174	5.96E-12	11.22	1.85
CAGGGG	617	444	173	1.11E-07	6.96	1.83
GGCTGA	602	430	172	7.89E-08	7.10	1.83
AGGAGC	643	471	172	2.55E-07	6.59	1.82
AAGGAG	738	567	171	2.05E-06	5.69	1.82
ACTGGG	640	469	171	2.59E-07	6.59	1.82
GACAGG	629	458	171	2.12E-07	6.67	1.81
CCTCTG	972	802	170	5.32E-05	4.27	1.80
GTGAGA	584	414	170	7.25E-08	7.14	1.80
CAGAGA	917	747	170	3.09E-05	4.51	1.80
GAGGCA	623	454	169	2.40E-07	6.62	1.80
GATGGG	573	404	169	5.95E-08	7.23	1.80
GAGGGC	532	363	169	1.50E-08	7.82	1.80
GAAAGA	797	628	169	7.69E-06	5.11	1.79
GCTGGC	634	465	169	3.58E-07	6.45	1.79
TTGGTG	612	444	168	2.22E-07	6.65	1.78
TGGAGC	599	431	168	1.62E-07	6.79	1.78
AGATGG	684	516	168	1.28E-06	5.89	1.78
AGAGGC	660	492	168	7.98E-07	6.10	1.78
AGGTGG	673	506	167	1.10E-06	5.96	1.77
GTAGAA	518	352	166	1.79E-08	7.75	1.76
TCTGAG	840	674	166	2.02E-05	4.69	1.76
GAAGGC	574	409	165	1.30E-07	6.88	1.75
GCTGTA	510	346	164	1.91E-08	7.72	1.74
AGGGTG	626	462	164	6.50E-07	6.19	1.74
AGGATG	637	473	164	8.63E-07	6.06	1.74
AGTGGG	649	485	164	1.20E-06	5.92	1.73
GTGGGC	528	365	163	4.57E-08	7.34	1.73
CAGCAG	943	782	161	1.01E-04	3.99	1.71
AGGGCA	644	483	161	1.56E-06	5.81	1.71
ACTGGA	616	456	160	9.82E-07	6.01	1.70
GACAGA	688	528	160	4.52E-06	5.35	1.70
GAGACA	654	496	158	2.95E-06	5.53	1.68

GGGATG	561	403	158	3.86E-07	6.41	1.67
GAGACC	485	328	157	3.34E-08	7.48	1.67
GGGAGC	552	395	157	3.16E-07	6.50	1.67
TGTGAC	634	477	157	2.40E-06	5.62	1.67
GGGGGC	457	300	157	1.18E-08	7.93	1.66
GGTGTG	641	484	157	2.90E-06	5.54	1.66
GTGTGA	632	476	156	2.58E-06	5.59	1.66
GAGAAC	521	365	156	1.48E-07	6.83	1.66
CCTGGG	946	790	156	1.76E-04	3.76	1.66
CTGAAG	806	650	156	4.24E-05	4.37	1.66
ATGTGG	618	462	156	2.05E-06	5.69	1.65
GAATGT	602	447	155	1.61E-06	5.79	1.65
AGCAGG	778	624	154	3.91E-05	4.41	1.63
AACTGT	663	509	154	6.99E-06	5.16	1.63
AGTGGA	582	428	154	1.37E-06	5.86	1.63
GGTTGG	501	348	153	1.58E-07	6.80	1.62
CTCTGG	893	740	153	1.59E-04	3.80	1.62
GAGGCT	630	478	152	4.94E-06	5.31	1.61
GACCTG	558	406	152	1.01E-06	5.99	1.61
GAGAGC	568	417	151	1.59E-06	5.80	1.60
GACTTG	535	385	150	7.58E-07	6.12	1.59
GTGACT	587	438	149	3.10E-06	5.51	1.58
GGGCTC	539	390	149	9.72E-07	6.01	1.58
TGGGGT	670	521	149	1.59E-05	4.80	1.58
GCTGCA	610	461	149	5.37E-06	5.27	1.58
AGGGAA	772	624	148	7.08E-05	4.15	1.57
TTGGGA	634	486	148	9.61E-06	5.02	1.57
AGAAAG	964	816	148	4.62E-04	3.34	1.57
GAAGAC	553	406	147	1.97E-06	5.70	1.56
AAAGGG	632	485	147	1.05E-05	4.98	1.56
AGAACT	654	507	147	1.58E-05	4.80	1.56
TTTGGG	732	585	147	5.07E-05	4.29	1.56
AGTGTG	751	604	147	6.49E-05	4.19	1.56
GAGGGT	507	360	147	6.03E-07	6.22	1.56
AAGAAG	781	634	147	9.37E-05	4.03	1.56
GCCTTA	414	268	146	2.01E-08	7.70	1.55
GGGACC	459	313	146	1.56E-07	6.81	1.55
TGAAGA	798	653	145	1.38E-04	3.86	1.54
GGGCTT	553	408	145	2.91E-06	5.54	1.54
TGGGCA	644	499	145	1.88E-05	4.73	1.53
GTGGCA	539	396	143	3.04E-06	5.52	1.51
AGAGTG	603	461	142	1.32E-05	4.88	1.51
GGGTGT	522	380	142	2.26E-06	5.65	1.51
AGGACA	701	559	142	6.33E-05	4.20	1.51
GAGATG	622	481	141	2.10E-05	4.68	1.50
GAGTGT	522	382	140	3.38E-06	5.47	1.48
CCTGGA	770	631	139	1.99E-04	3.70	1.48
GGACCT	460	321	139	6.46E-07	6.19	1.47
CTGGCA	632	493	139	3.39E-05	4.47	1.47
CTTGGG	691	552	139	8.29E-05	4.08	1.47
GGTGAG	552	413	139	8.19E-06	5.09	1.47
ATGGAG	611	473	138	2.97E-05	4.53	1.46
TGAATG	631	495	136	5.00E-05	4.30	1.44
GCTCTG	835	699	136	5.17E-04	3.29	1.44

CTCTGA	799	663	136	3.82E-04	3.42	1.44
GGACTT	499	364	135	4.16E-06	5.38	1.43
TGTGGT	697	562	135	1.45E-04	3.84	1.43
AGAGCA	713	578	135	1.76E-04	3.75	1.43
GGATGA	454	320	134	1.38E-06	5.86	1.42
CTGAAC	498	364	134	5.26E-06	5.28	1.42
GTTGGA	435	302	133	8.83E-07	6.05	1.41
TCTGGA	716	583	133	2.18E-04	3.66	1.41
AAGGAC	535	403	132	1.60E-05	4.80	1.40
ACAGGA	698	566	132	2.11E-04	3.68	1.40
TTGTAG	496	365	131	8.31E-06	5.08	1.39
CAGAGC	772	642	130	5.20E-04	3.28	1.38
TGAGTG	620	490	130	9.13E-05	4.04	1.38
GATTGT	415	285	130	8.59E-07	6.07	1.38
CTCTGT	920	790	130	1.67E-03	2.78	1.38
GGACCA	465	336	129	4.99E-06	5.30	1.37
CAGTGG	703	574	129	3.05E-04	3.52	1.37
TACTGT	593	464	129	7.26E-05	4.14	1.37
GAAGTG	574	445	129	5.57E-05	4.25	1.36
TCAGGG	613	484	129	1.04E-04	3.98	1.36
CAGAAG	832	703	129	1.04E-03	2.98	1.36
GTGAAG	570	442	128	5.45E-05	4.26	1.36
TGAGAA	787	660	127	8.07E-04	3.09	1.35
GTGGGG	581	454	127	7.89E-05	4.10	1.35
GTGGGT	557	430	127	5.60E-05	4.25	1.34
GGACTC	442	316	126	4.36E-06	5.36	1.34
GCAGCT	648	522	126	2.19E-04	3.66	1.34
GAAGCA	651	525	126	2.33E-04	3.63	1.34
GAGCCA	613	487	126	1.43E-04	3.84	1.34
CAGGGC	664	538	126	2.86E-04	3.54	1.33
ATGGGG	508	382	126	2.50E-05	4.60	1.33
CTGCAG	901	775	126	2.15E-03	2.67	1.33
ACTCTG	678	553	125	3.49E-04	3.46	1.33
TTTGGG	698	573	125	4.65E-04	3.33	1.32
GGAACT	480	356	124	1.69E-05	4.77	1.32
GGGGAT	397	273	124	1.55E-06	5.81	1.32
TTGGAG	591	467	124	1.33E-04	3.88	1.32
GATGTG	542	418	124	6.36E-05	4.20	1.31
GCTGGT	520	397	123	5.18E-05	4.29	1.30
GGCAAG	472	350	122	2.05E-05	4.69	1.29
GGGTTG	440	318	122	9.44E-06	5.03	1.29
TGGGAT	539	417	122	8.38E-05	4.08	1.29
GGAGGT	488	367	121	3.23E-05	4.49	1.29
CCTGGC	715	594	121	8.07E-04	3.09	1.28
GGGGGT	463	342	121	2.05E-05	4.69	1.28
AGAACG	657	536	121	4.84E-04	3.32	1.28
GGGGCC	446	326	120	1.46E-05	4.84	1.28
ACTGTT	640	520	120	4.07E-04	3.39	1.28
CAAGGG	502	382	120	5.73E-05	4.24	1.27
CAGGAC	576	456	120	1.97E-04	3.70	1.27
GGTGGC	506	387	119	6.33E-05	4.20	1.27
GGGCCA	503	384	119	6.19E-05	4.21	1.26
AAGGAA	903	784	119	3.76E-03	2.43	1.26
CCAAGG	603	484	119	3.14E-04	3.50	1.26

GGAATG	513	394	119	8.23E-05	4.08	1.26
GCAGCA	622	503	119	4.07E-04	3.39	1.26
AGAGCT	681	563	118	7.82E-04	3.11	1.26
GACTGC	421	303	118	1.16E-05	4.93	1.25
GTAGGG	355	237	118	1.36E-06	5.87	1.25
GTAGGA	389	271	118	4.77E-06	5.32	1.25
GATGAG	467	350	117	3.98E-05	4.40	1.24
AAGATG	675	558	117	8.33E-04	3.08	1.24
GTCTGT	685	568	117	9.46E-04	3.02	1.24
GCTGTT	627	510	117	5.19E-04	3.28	1.24
GCAGAC	449	332	117	3.07E-05	4.51	1.24
CTGGCC	683	567	116	9.92E-04	3.00	1.23
GGATGT	459	343	116	4.35E-05	4.36	1.23
GGAGCC	553	437	116	2.35E-04	3.63	1.23
GAAGAT	528	413	115	1.67E-04	3.78	1.22
TGGAAC	452	337	115	4.08E-05	4.39	1.22
TGGACC	405	290	115	1.24E-05	4.91	1.22
ACACTG	694	579	115	1.28E-03	2.89	1.22
GTAGAC	320	206	114	6.33E-07	6.20	1.21
GGTGGT	479	365	114	8.98E-05	4.05	1.21
TGAGCA	614	501	113	6.77E-04	3.17	1.20
AGCTGT	739	626	113	2.17E-03	2.66	1.20
GGGGGG	636	523	113	8.86E-04	3.05	1.20
TTGGAC	365	252	113	5.33E-06	5.27	1.20
AGAACCC	473	360	113	9.21E-05	4.04	1.20
TGGTGA	569	456	113	4.26E-04	3.37	1.20
GCAGTG	633	521	112	9.57E-04	3.02	1.19
CAGCTG	850	738	112	4.98E-03	2.30	1.19
AGGACC	466	354	112	9.36E-05	4.03	1.19
AGCCAG	790	678	112	3.51E-03	2.46	1.19
GGGATT	396	285	111	1.94E-05	4.71	1.18
GAGAGT	460	349	111	9.09E-05	4.04	1.18
GAGGAT	417	306	111	3.49E-05	4.46	1.18
GCAAGG	463	352	111	1.00E-04	4.00	1.18
AAGGTG	531	420	111	3.27E-04	3.49	1.17
GGGTGA	457	346	111	9.45E-05	4.02	1.17
ACTGAA	639	529	110	1.26E-03	2.90	1.17
GAACTC	405	296	109	3.54E-05	4.45	1.16
GTGTAG	395	286	109	2.82E-05	4.55	1.16
AGGTGC	414	306	108	5.74E-05	4.24	1.14
GAGTTG	440	332	108	1.03E-04	3.99	1.14
GGGAAC	428	321	107	8.54E-05	4.07	1.14
CCAGAG	797	690	107	5.39E-03	2.27	1.14
GTTGGT	424	317	107	8.25E-05	4.08	1.14
ATGCTG	636	529	107	1.70E-03	2.77	1.14
GCCAGG	674	567	107	2.42E-03	2.62	1.13
ATGGGA	538	431	107	6.15E-04	3.21	1.13
GACCTC	405	299	106	6.00E-05	4.22	1.13
CAAGGA	579	473	106	1.05E-03	2.98	1.13
AACTGG	494	388	106	3.62E-04	3.44	1.12
AGCAGC	690	584	106	3.04E-03	2.52	1.12
ACAGAG	751	645	106	4.68E-03	2.33	1.12
TGAACT	541	435	106	7.33E-04	3.13	1.12
GTGGAT	412	307	105	8.32E-05	4.08	1.12

TGTGCC	590	485	105	1.33E-03	2.88	1.12
GAGTGA	470	366	104	3.08E-04	3.51	1.11
GACAAG	461	357	104	2.66E-04	3.58	1.11
GCAGAA	605	501	104	1.78E-03	2.75	1.10
GCTGAA	503	399	104	5.55E-04	3.26	1.10
TGGAGT	558	454	104	1.14E-03	2.94	1.10
GCTTTG	680	577	103	3.56E-03	2.45	1.10
GGAACA	513	410	103	6.74E-04	3.17	1.09
TGAACC	377	274	103	5.26E-05	4.28	1.09
GTGGCC	510	407	103	6.77E-04	3.17	1.09
TGCAGG	619	516	103	2.28E-03	2.64	1.09
CCAGGG	730	627	103	5.28E-03	2.28	1.09
ACCTGT	555	453	102	1.31E-03	2.88	1.08
GGATGC	403	301	102	1.22E-04	3.92	1.08
GTGTTG	513	412	101	8.84E-04	3.05	1.07
ACTTGA	529	428	101	1.09E-03	2.96	1.07
ACCTGG	568	467	101	1.69E-03	2.77	1.07
TGTAGC	427	326	101	2.50E-04	3.60	1.07
AGGGGT	447	347	100	3.66E-04	3.44	1.06
GGTCTG	505	405	100	8.80E-04	3.06	1.06
GCAGGC	519	419	100	1.06E-03	2.98	1.06
GGAAGC	586	486	100	2.19E-03	2.66	1.06
CCTGAG	741	641	100	7.37E-03	2.13	1.06
GACTCT	498	399	99	9.22E-04	3.04	1.05
AGTAGA	442	343	99	4.11E-04	3.39	1.05
TGTCTG	846	747	99	1.31E-02	1.88	1.05
CGTGTG	265	166	99	2.03E-06	5.69	1.05
GTTGTG	460	361	99	5.81E-04	3.24	1.05
GGCCAG	635	537	98	4.12E-03	2.39	1.04
TGAGCC	531	433	98	1.64E-03	2.79	1.04
CTGGCT	790	692	98	1.13E-02	1.95	1.03
GGCAGT	484	387	97	9.60E-04	3.02	1.03
GAGGCC	501	404	97	1.25E-03	2.90	1.03
TGTTTG	909	812	97	1.93E-02	1.71	1.03
TGCAGA	685	588	97	6.59E-03	2.18	1.03
GGACAA	413	316	97	3.41E-04	3.47	1.03
GGGTGC	373	277	96	1.59E-04	3.80	1.02
TGTTGA	539	443	96	2.16E-03	2.67	1.02
TGAGAC	473	378	95	1.06E-03	2.97	1.01
GGGAGT	424	329	95	5.24E-04	3.28	1.01
AAGTGG	519	424	95	1.99E-03	2.70	1.01
TGATGG	524	429	95	2.14E-03	2.67	1.00
CCCTGG	768	673	95	1.26E-02	1.90	1.00
AGGGAT	447	352	95	8.06E-04	3.09	1.00
TGCTGA	656	562	94	6.84E-03	2.16	1.00
CTGCC	768	674	94	1.31E-02	1.88	1.00
CTGTCC	715	621	94	9.97E-03	2.00	1.00
GGGGTC	363	269	94	1.87E-04	3.73	1.00
TTGCTG	701	607	94	9.40E-03	2.03	1.00
CTGTAC	435	341	94	7.60E-04	3.12	0.99
GAGCAA	442	348	94	8.78E-04	3.06	0.99
CTTGAA	585	492	93	4.40E-03	2.36	0.99
GAACCT	404	311	93	4.83E-04	3.32	0.99
CTGGAA	737	644	93	1.23E-02	1.91	0.99

GGCACT	412	319	93	6.12E-04	3.21	0.98
ATGTAG	433	341	92	8.82E-04	3.05	0.98
GAACAG	536	444	92	3.35E-03	2.47	0.97
GTGAGC	448	357	91	1.27E-03	2.90	0.97
GGGAAA	696	605	91	1.14E-02	1.94	0.97
GTGAAC	370	279	91	3.47E-04	3.46	0.97
CTTTGG	683	592	91	1.08E-02	1.97	0.96
AGTGGC	472	381	91	1.85E-03	2.73	0.96
GATTGG	314	223	91	9.20E-05	4.04	0.96
GAGCTC	440	350	90	1.28E-03	2.89	0.96
GTCAGG	477	387	90	2.12E-03	2.67	0.96
AGAGGT	507	417	90	2.98E-03	2.53	0.96
GGACCC	373	283	90	4.58E-04	3.34	0.95
GAATGG	461	371	90	1.88E-03	2.73	0.95
GCCTGT	600	510	90	7.11E-03	2.15	0.95
GACAGC	484	395	89	2.81E-03	2.55	0.94
CAGGAA	804	715	89	2.31E-02	1.64	0.94
AGAATG	625	537	88	9.51E-03	2.02	0.94
AAGGCC	602	514	88	8.16E-03	2.09	0.94
GGTAGA	372	284	88	5.68E-04	3.25	0.94
ATGGAC	370	282	88	5.47E-04	3.26	0.94
AAGCTG	667	579	88	1.25E-02	1.90	0.93
TTGGAT	441	353	88	1.83E-03	2.74	0.93
TGCCTG	792	705	87	2.44E-02	1.61	0.92
GTTCTG	626	539	87	1.09E-02	1.96	0.92
TGGGCC	479	392	87	3.36E-03	2.47	0.92
GTACTG	366	280	86	6.65E-04	3.18	0.92
AGCTGC	630	544	86	1.16E-02	1.93	0.92
TGGACG	160	74	86	1.55E-08	7.81	0.92
CAGACT	563	477	86	7.67E-03	2.12	0.91
GACCCC	346	260	86	4.80E-04	3.32	0.91
GCTGCC	619	533	86	1.14E-02	1.94	0.91
GCTTGG	494	408	86	4.26E-03	2.37	0.91
AGGGCC	464	378	86	3.12E-03	2.51	0.91
GGTAGG	357	271	86	6.25E-04	3.20	0.91
AGCTGA	606	520	86	1.08E-02	1.97	0.91
AAGACT	537	452	85	6.54E-03	2.18	0.91
AGGAAC	498	413	85	4.64E-03	2.33	0.91
AGCCTG	751	666	85	2.32E-02	1.63	0.91
GGACGA	140	55	85	1.16E-09	8.94	0.90
AAGAAC	528	444	84	6.73E-03	2.17	0.90
CATGGG	494	410	84	5.27E-03	2.28	0.89
GTGATG	473	390	83	4.53E-03	2.34	0.88
AAAGAG	679	596	83	2.07E-02	1.68	0.88
GCCCTG	692	610	82	2.24E-02	1.65	0.87
GCCTGA	485	403	82	5.86E-03	2.23	0.87
GGTGAC	403	321	82	2.31E-03	2.64	0.87
TAGAAC	365	283	82	1.29E-03	2.89	0.87
GATGCT	515	433	82	7.88E-03	2.10	0.87
GACCAG	446	364	82	4.08E-03	2.39	0.87
TGGCAT	485	403	82	6.15E-03	2.21	0.87
CTCTGC	803	721	82	3.65E-02	1.44	0.87
TGGTGT	580	498	82	1.30E-02	1.89	0.86
CGAGGA	185	104	81	1.72E-06	5.76	0.86

G TGCTT	547	466	81	1.11E-02	1.96	0.86
A TGGTG	486	405	81	6.84E-03	2.16	0.86
T TGAGGC	485	404	81	6.81E-03	2.17	0.86
G GGGACG	164	83	81	3.04E-07	6.52	0.85
A AGAACAA	668	588	80	2.34E-02	1.63	0.85
G GTCTGG	499	419	80	8.04E-03	2.09	0.85
C CCAGGA	733	653	80	3.10E-02	1.51	0.85
A ACTTGG	521	441	80	9.74E-03	2.01	0.85
G GGCTCT	596	516	80	1.67E-02	1.78	0.85
G GATGGT	394	314	80	2.74E-03	2.56	0.85
G GAGCCC	470	390	80	6.71E-03	2.17	0.84
T TTGAGG	467	388	79	6.58E-03	2.18	0.84
A AAAGGA	775	696	79	3.86E-02	1.41	0.84
G GGCTTG	474	395	79	7.24E-03	2.14	0.84
C CACTGG	616	537	79	1.99E-02	1.70	0.84
T TAGAGA	506	427	79	9.81E-03	2.01	0.84
G GAACCC	335	256	79	1.21E-03	2.92	0.83
A AGTTGG	429	350	79	4.86E-03	2.31	0.83
A AGGAAA	931	853	78	6.31E-02	1.20	0.83
T TTCTGG	725	647	78	3.42E-02	1.47	0.83
C CTGGAT	488	410	78	8.89E-03	2.05	0.83
G GTGCTA	339	261	78	1.43E-03	2.84	0.83
G GCAGCC	558	480	78	1.56E-02	1.81	0.83
G GGAGAT	427	349	78	5.22E-03	2.28	0.82
A AGAGCC	583	505	78	1.84E-02	1.74	0.82
G GAAGGT	446	368	78	6.46E-03	2.19	0.82
C CTGACC	483	406	77	9.36E-03	2.03	0.82
C CTTGGA	557	480	77	1.64E-02	1.79	0.82
G GGCGGG	232	155	77	9.27E-05	4.03	0.82
C CCCTCC	758	681	77	4.26E-02	1.37	0.82
T TTGAAG	578	501	77	1.94E-02	1.71	0.81
C CACCTG	603	526	77	2.27E-02	1.64	0.81
C CAGAAC	529	453	76	1.48E-02	1.83	0.81
G GGGCAA	352	276	76	2.32E-03	2.63	0.81
G GAAGCC	532	456	76	1.54E-02	1.81	0.81
G GGTTTG	504	428	76	1.28E-02	1.89	0.81
G GAACCA	402	326	76	4.91E-03	2.31	0.80
T TGGATT	477	401	76	1.06E-02	1.97	0.80
G GAACAA	450	374	76	8.43E-03	2.07	0.80
G GGCATG	397	321	76	4.82E-03	2.32	0.80
G GGAAGT	511	435	76	1.41E-02	1.85	0.80
T TGCACT	466	391	75	1.04E-02	1.98	0.80
C CGTGGAA	190	115	75	1.79E-05	4.75	0.79
G GCATGG	421	346	75	6.90E-03	2.16	0.79
T TAGAGG	399	324	75	5.42E-03	2.27	0.79
A AGTGAG	563	488	75	2.13E-02	1.67	0.79
G GCCTTG	542	467	75	1.88E-02	1.73	0.79
G GTAGGC	257	183	74	3.82E-04	3.42	0.79
C CCTTGG	621	547	74	2.94E-02	1.53	0.79
G GTAGAT	313	239	74	1.53E-03	2.82	0.79
G GCTGTC	525	451	74	1.73E-02	1.76	0.79
T TAGGAG	393	319	74	5.48E-03	2.26	0.79
G GAGAAA	808	734	74	5.94E-02	1.23	0.78
G GAATTG	371	297	74	4.19E-03	2.38	0.78

GGTGCC	367	293	74	4.03E-03	2.39	0.78
AGTGAC	468	394	74	1.20E-02	1.92	0.78
GGGCCT	481	407	74	1.34E-02	1.87	0.78
GCCCCT	503	429	74	1.58E-02	1.80	0.78
TTGGGC	370	297	73	4.42E-03	2.35	0.78
AGATTG	373	300	73	4.65E-03	2.33	0.78
TAGGAC	298	225	73	1.33E-03	2.87	0.78
AGTGCC	422	349	73	8.38E-03	2.08	0.78
GACCAA	341	268	73	3.02E-03	2.52	0.78
GGTGCA	334	261	73	2.80E-03	2.55	0.77
GCACAG	597	525	72	3.18E-02	1.50	0.76
GGGTAG	344	272	72	3.85E-03	2.41	0.76
GACACT	441	369	72	1.18E-02	1.93	0.76
GCAGGG	208	136	72	1.16E-04	3.93	0.76
GAATGA	461	390	71	1.47E-02	1.83	0.75
GGCCCA	431	360	71	1.16E-02	1.93	0.75
CGGGGC	198	127	71	8.51E-05	4.07	0.75
CGTGGG	207	136	71	1.31E-04	3.88	0.75
GTAGTG	305	234	71	2.35E-03	2.63	0.75
GAGCCT	543	473	70	2.81E-02	1.55	0.74
GGACAT	391	321	70	8.74E-03	2.06	0.74
CGGCTG	191	122	69	8.79E-05	4.06	0.74
GAACAC	406	337	69	1.11E-02	1.96	0.73
GGGGTT	396	327	69	1.02E-02	1.99	0.73
GGACAC	415	346	69	1.23E-02	1.91	0.73
CGCAGA	151	82	69	6.04E-06	5.22	0.73
TGAAGC	498	429	69	2.36E-02	1.63	0.73
CTGCAC	484	415	69	2.16E-02	1.67	0.73
CAAGAG	516	447	69	2.64E-02	1.58	0.73
TGGTTG	451	382	69	1.71E-02	1.77	0.73
GGCATT	385	316	69	9.40E-03	2.03	0.73
GCTGCG	177	109	68	5.47E-05	4.26	0.72
GGCTCC	501	433	68	2.57E-02	1.59	0.72
GGGCC	372	304	68	8.82E-03	2.05	0.72
TGAGCT	568	500	68	3.83E-02	1.42	0.72
GTGACA	502	434	68	2.71E-02	1.57	0.72
GACGTG	156	89	67	1.77E-05	4.75	0.71
TGAACG	141	74	67	4.79E-06	5.32	0.71
ACCTCT	501	434	67	2.84E-02	1.55	0.71
TGATTG	389	322	67	1.21E-02	1.92	0.71
GTGCAG	497	430	67	2.81E-02	1.55	0.71
GTGAAT	415	348	67	1.56E-02	1.81	0.71
TCACTG	654	587	67	5.84E-02	1.23	0.71
ACAGGG	518	451	67	3.24E-02	1.49	0.71
AGGACG	157	91	66	2.38E-05	4.62	0.70
ATTGGG	319	253	66	5.64E-03	2.25	0.70
TTGGAA	635	569	66	5.68E-02	1.25	0.70
GAGTGC	325	259	66	6.27E-03	2.20	0.70
GACGGG	141	75	66	7.21E-06	5.14	0.70
GCCAAG	480	414	66	2.76E-02	1.56	0.70
GTTGAG	357	291	66	9.66E-03	2.01	0.70
AACTGA	515	449	66	3.41E-02	1.47	0.70
GGTGAA	375	310	65	1.24E-02	1.90	0.69
CAGGCG	168	103	65	7.34E-05	4.13	0.69

GGGCAC	360	295	65	1.08E-02	1.97	0.69
TCTCTG	927	862	65	1.23E-01	0.91	0.69
ATGAGA	501	437	64	3.57E-02	1.45	0.68
CTGCCT	927	863	64	1.29E-01	0.89	0.68
CGGGAG	191	127	64	3.19E-04	3.50	0.68
GGCGTG	165	101	64	8.47E-05	4.07	0.68
CTCGGA	156	92	64	5.01E-05	4.30	0.68
AAGAGC	481	417	64	3.34E-02	1.48	0.68
CCCCTC	597	533	64	5.80E-02	1.24	0.68
GTGAGT	420	356	64	2.25E-02	1.65	0.67
CGGGCT	168	104	64	1.18E-04	3.93	0.67
GGACGG	146	82	64	2.62E-05	4.58	0.67
CGGGCA	157	94	63	6.53E-05	4.19	0.67
GTGTCT	621	558	63	6.76E-02	1.17	0.67
AGACAG	701	638	63	8.64E-02	1.06	0.67
TGGGTT	557	495	62	5.41E-02	1.27	0.66
AGGAGT	453	391	62	3.19E-02	1.50	0.66
GGTCAG	463	401	62	3.45E-02	1.46	0.66
AGACCC	403	341	62	2.32E-02	1.64	0.66
CAGGTG	577	515	62	6.13E-02	1.21	0.66
GGGCAT	344	282	62	1.36E-02	1.87	0.65
ATGGGC	340	278	62	1.32E-02	1.88	0.65
AGGCCG	165	103	62	1.72E-04	3.76	0.65
TTGGGT	479	417	62	3.99E-02	1.40	0.65
AGACCA	447	386	61	3.32E-02	1.48	0.65
GATGGC	369	308	61	1.82E-02	1.74	0.65
TGCAGC	520	459	61	4.97E-02	1.30	0.65
GCCCAG	652	591	61	8.18E-02	1.09	0.65
CGAGAG	149	88	61	6.84E-05	4.17	0.65
TAGGGG	287	226	61	6.96E-03	2.16	0.65
AACCTG	475	414	61	4.06E-02	1.39	0.65
CCCAGG	796	735	61	1.19E-01	0.93	0.65
GAGCGG	151	90	61	8.87E-05	4.05	0.65
AGATGA	549	488	61	5.89E-02	1.23	0.64
CCTGCC	783	722	61	1.17E-01	0.93	0.64
ATTGTG	466	405	61	3.96E-02	1.40	0.64
TAAGGG	313	252	61	1.09E-02	1.96	0.64
ATTGGA	348	288	60	1.64E-02	1.78	0.64
CGGAGG	176	116	60	4.06E-04	3.39	0.64
ACGTGG	182	122	60	5.47E-04	3.26	0.64
GTGTGC	532	472	60	5.73E-02	1.24	0.64
GGGAAT	385	325	60	2.41E-02	1.62	0.64
TTGAAC	367	307	60	2.10E-02	1.68	0.64
ACTGAC	399	339	60	2.76E-02	1.56	0.63
TGGCCT	649	589	60	8.93E-02	1.05	0.63
GAGCAC	380	321	59	2.48E-02	1.61	0.63
CCCCTG	566	507	59	6.98E-02	1.16	0.63
ACCGTG	171	112	59	4.21E-04	3.38	0.63
AGACGG	146	87	59	1.08E-04	3.97	0.63
GGGTCT	428	369	59	3.64E-02	1.44	0.63
GACCGT	119	60	59	1.15E-05	4.94	0.62
CTGGGT	636	577	59	9.24E-02	1.03	0.62
GTGACC	388	330	58	2.90E-02	1.54	0.62
GGTTGT	360	302	58	2.31E-02	1.64	0.62

AGACAC	488	430	58	5.39E-02	1.27	0.62
GGGGTA	257	199	58	6.34E-03	2.20	0.62
CCGAGG	195	137	58	1.39E-03	2.86	0.62
CCCCAG	735	677	58	1.21E-01	0.92	0.62
CGGAGA	147	89	58	1.52E-04	3.82	0.62
GATGAA	441	383	58	4.27E-02	1.37	0.62
AGCGGG	154	96	58	2.37E-04	3.62	0.62
GCAGAT	404	346	58	3.39E-02	1.47	0.62
GGAGCG	150	92	58	1.94E-04	3.71	0.61
AGAACG	147	89	58	1.73E-04	3.76	0.61
GGCCCC	377	320	57	2.95E-02	1.53	0.61
TGTGCT	734	677	57	1.27E-01	0.90	0.61
TGTACA	540	483	57	7.45E-02	1.13	0.60
GGCCAC	426	369	57	4.31E-02	1.37	0.60
CCGTGG	207	150	57	2.56E-03	2.59	0.60
GCAATA	274	217	57	1.02E-02	1.99	0.60
GGCTTT	603	547	56	9.59E-02	1.02	0.60
GAACGG	125	69	56	5.04E-05	4.30	0.60
GGCGGC	154	98	56	3.85E-04	3.41	0.60
AGGTTG	382	326	56	3.50E-02	1.46	0.59
CTGCCG	186	130	56	1.60E-03	2.79	0.59
AGGTAG	369	313	56	3.18E-02	1.50	0.59
GATTG	425	369	56	4.69E-02	1.33	0.59
GGCGAG	139	83	56	1.86E-04	3.73	0.59
GGACGT	121	65	56	4.55E-05	4.34	0.59
TGGCCA	583	527	56	9.52E-02	1.02	0.59
CGGAGC	155	99	56	4.94E-04	3.31	0.59
GGAACC	338	282	56	2.58E-02	1.59	0.59
TCGGGG	154	99	55	4.79E-04	3.32	0.59
GAGTAG	302	247	55	1.80E-02	1.74	0.59
ACCAAG	444	389	55	5.50E-02	1.26	0.59
GGCCGG	153	98	55	4.72E-04	3.33	0.59
GACATG	402	347	55	4.34E-02	1.36	0.59
TAGGGC	257	202	55	9.93E-03	2.00	0.59
TGGCCC	461	406	55	6.10E-02	1.21	0.58
CCGGGC	160	105	55	7.14E-04	3.15	0.58
GAAGCT	518	463	55	7.90E-02	1.10	0.58
TCGGAG	136	81	55	1.97E-04	3.70	0.58
AGACGT	142	87	55	3.00E-04	3.52	0.58
GTTGAA	378	324	54	3.99E-02	1.40	0.58
CGGCAG	160	106	54	8.59E-04	3.07	0.58
CACTGA	580	526	54	1.03E-01	0.99	0.58
ACTGGC	395	341	54	4.61E-02	1.34	0.57
CGGGGT	147	93	54	5.11E-04	3.29	0.57
TGACCT	498	444	54	7.94E-02	1.10	0.57
CCGGGG	169	115	54	1.47E-03	2.83	0.57
AATGTG	608	554	54	1.16E-01	0.94	0.57
GTAGCA	319	265	54	2.68E-02	1.57	0.57
TGGGCG	154	101	53	8.03E-04	3.10	0.57
ACTGCA	487	434	53	7.80E-02	1.11	0.57
AACTTG	473	420	53	7.43E-02	1.13	0.57
CCACTG	609	556	53	1.19E-01	0.92	0.56
GAACGA	111	58	53	4.33E-05	4.36	0.56
CCGTGT	194	141	53	3.71E-03	2.43	0.56

GGATT	459	406	53	7.11E-02	1.15	0.56
AGCGAG	152	99	53	8.12E-04	3.09	0.56
AGGTGA	483	430	53	8.06E-02	1.09	0.56
GATTGA	260	207	53	1.47E-02	1.83	0.56
GTGACG	123	70	53	1.56E-04	3.81	0.56
CCTGAA	548	496	52	1.04E-01	0.98	0.56
CTCGGG	189	137	52	3.81E-03	2.42	0.55
TGAGCG	138	86	52	5.10E-04	3.29	0.55
TGGCCG	148	96	52	8.87E-04	3.05	0.55
AGCAAG	545	493	52	1.07E-01	0.97	0.55
GAGACG	139	87	52	5.60E-04	3.25	0.55
GGGTTT	514	462	52	9.71E-02	1.01	0.55
GCGTGG	163	111	52	1.77E-03	2.75	0.55
GGGCCG	143	91	52	7.18E-04	3.14	0.55
CTGAAT	482	430	52	8.72E-02	1.06	0.55
GCAAGA	383	332	51	5.41E-02	1.27	0.55
ACTGGT	382	331	51	5.38E-02	1.27	0.55
TGTGCG	159	108	51	1.65E-03	2.78	0.54
GGGCTA	259	208	51	1.76E-02	1.75	0.54
CGGATG	125	74	51	2.80E-04	3.55	0.54
CCCGGG	194	143	51	5.36E-03	2.27	0.54
TTGAGC	346	295	51	4.35E-02	1.36	0.54
TGGCGG	143	92	51	8.75E-04	3.06	0.54
ATGCAG	487	436	51	9.39E-02	1.03	0.54
TGTCGG	117	66	51	1.78E-04	3.75	0.54
GGCCAT	367	316	51	5.23E-02	1.28	0.54
GGAACG	125	74	51	3.38E-04	3.47	0.54
TGCACC	316	266	50	3.66E-02	1.44	0.53
CTGTAA	525	475	50	1.11E-01	0.95	0.53
GCGGAG	142	92	50	1.00E-03	3.00	0.53
AGGGCG	147	97	50	1.28E-03	2.89	0.53
GCAGGT	427	377	50	7.62E-02	1.12	0.53
ACCTGA	441	391	50	8.24E-02	1.08	0.53
TCTGCC	658	608	50	1.59E-01	0.80	0.53
CGGAAG	154	104	50	1.86E-03	2.73	0.53
CAGAGT	581	531	50	1.34E-01	0.87	0.53
ACGGAG	142	92	50	1.19E-03	2.93	0.53
CCCCGG	167	118	49	3.34E-03	2.48	0.52
TGAACA	526	477	49	1.18E-01	0.93	0.52
CGGTGG	157	108	49	2.35E-03	2.63	0.52
GTGGCG	133	84	49	8.63E-04	3.06	0.52
GTCCTG	575	526	49	1.39E-01	0.86	0.52
GTGCC	380	331	49	6.58E-02	1.18	0.52
AGACCT	458	409	49	9.59E-02	1.02	0.52
GGGATA	260	211	49	2.43E-02	1.61	0.52
AACGGA	119	70	49	4.20E-04	3.38	0.51
AAGGCC	420	372	48	8.48E-02	1.07	0.51
CCTCCC	770	722	48	2.09E-01	0.68	0.51
CGGACA	114	66	48	3.16E-04	3.50	0.51
CCGGAG	152	104	48	2.53E-03	2.60	0.51
CTGCGG	171	123	48	4.88E-03	2.31	0.51
CGGGGA	168	120	48	4.47E-03	2.35	0.51
ACGCAG	133	85	48	1.09E-03	2.96	0.51
GATGCA	349	301	48	5.86E-02	1.23	0.51

GCTGAC	369	321	48	6.68E-02	1.18	0.51
GGTGT	420	372	48	8.76E-02	1.06	0.51
GCAGCG	161	113	48	3.83E-03	2.42	0.51
GCCGGA	113	66	47	3.87E-04	3.41	0.50
ACGGTG	143	96	47	2.23E-03	2.65	0.50
ACAAGG	425	378	47	9.69E-02	1.01	0.50
GCATGC	332	285	47	5.95E-02	1.23	0.50
CGCTGG	164	117	47	5.29E-03	2.28	0.50
TTAGGA	418	371	47	9.68E-02	1.01	0.49
GACGTT	117	70	47	6.67E-04	3.18	0.49
GCCGAG	146	99	47	2.98E-03	2.53	0.49
GTAGCT	343	297	46	6.60E-02	1.18	0.49
CCCTCT	633	587	46	1.84E-01	0.74	0.49
CGTAGA	99	53	46	1.63E-04	3.79	0.49
TCCCTC	618	572	46	1.78E-01	0.75	0.49
AGAGCG	144	98	46	2.84E-03	2.55	0.49
GACGAG	108	62	46	3.71E-04	3.43	0.49
AGCCGG	150	104	46	3.61E-03	2.44	0.49
GAGGCG	147	101	46	3.31E-03	2.48	0.49
GAAATG	670	624	46	1.99E-01	0.70	0.49
GAACCG	106	60	46	3.51E-04	3.45	0.49
CTGATG	507	461	46	1.39E-01	0.86	0.49
CGGGTG	145	99	46	3.30E-03	2.48	0.49
GACGAC	90	44	46	7.40E-05	4.13	0.49
CAGCGG	160	114	46	5.61E-03	2.25	0.49
GAACGT	118	72	46	8.88E-04	3.05	0.49
GACCAC	302	256	46	5.24E-02	1.28	0.49
CGGGGG	148	102	46	3.82E-03	2.42	0.49
TCTGTA	608	562	46	1.81E-01	0.74	0.48
GGCCAA	331	285	46	6.54E-02	1.18	0.48
TGCGTG	162	116	46	6.12E-03	2.21	0.48
GACCCT	391	345	46	9.20E-02	1.04	0.48
GACAGT	453	407	46	1.20E-01	0.92	0.48
GACGGC	99	54	45	2.51E-04	3.60	0.48
AGAAGT	556	511	45	1.66E-01	0.78	0.48
GCGAGG	127	82	45	1.87E-03	2.73	0.48
GGGCCG	194	149	45	1.53E-02	1.81	0.48
TGCCCC	461	416	45	1.30E-01	0.89	0.48
GAATCG	118	73	45	1.19E-03	2.92	0.48
TGACCG	112	67	45	8.24E-04	3.08	0.47
GCGTGT	149	104	45	5.01E-03	2.30	0.47
CGGGTT	115	70	45	1.04E-03	2.98	0.47
AATGGG	392	347	45	1.01E-01	0.99	0.47
AGAGAT	512	467	45	1.55E-01	0.81	0.47
GAGCGA	114	69	45	1.01E-03	3.00	0.47
GCCGTG	160	116	44	7.36E-03	2.13	0.47
GAATGC	321	277	44	6.92E-02	1.16	0.47
CGAGGG	144	100	44	4.45E-03	2.35	0.47
GATCGG	80	36	44	3.70E-05	4.43	0.47
TTGCAC	324	280	44	7.12E-02	1.15	0.47
CGGGAA	148	104	44	5.61E-03	2.25	0.47
AGGCCA	552	508	44	1.77E-01	0.75	0.47
GATTGC	224	180	44	2.92E-02	1.53	0.46
CTTTGA	625	581	44	2.09E-01	0.68	0.46

AGGCC	412	368	44	1.19E-01	0.92	0.46
GGAGTC	352	309	43	9.06E-02	1.04	0.46
GGCCGA	107	64	43	8.69E-04	3.06	0.46
GATGAC	300	257	43	6.55E-02	1.18	0.46
GAAGCG	125	82	43	2.51E-03	2.60	0.46
CGTGCT	162	119	43	9.52E-03	2.02	0.46
ACGGGA	128	85	43	3.03E-03	2.52	0.46
CGTGAG	144	101	43	5.98E-03	2.22	0.46
GCACCT	350	307	43	9.34E-02	1.03	0.46
TCTGAC	446	403	43	1.40E-01	0.85	0.46
GTACAG	364	321	43	1.01E-01	1.00	0.46
GATCTG	369	326	43	1.05E-01	0.98	0.45
GATGTA	313	270	43	7.71E-02	1.11	0.45
GGCGGT	119	76	43	2.28E-03	2.64	0.45
GCGCTG	156	113	43	9.55E-03	2.02	0.45
GCCGGG	152	110	42	8.78E-03	2.06	0.45
GCACGG	130	88	42	4.15E-03	2.38	0.45
CAGGAT	457	415	42	1.52E-01	0.82	0.45
ATACTG	376	334	42	1.13E-01	0.95	0.45
AAGCAG	669	627	42	2.41E-01	0.62	0.45
AAGACG	129	87	42	4.14E-03	2.38	0.45
TTTGTG	796	754	42	2.85E-01	0.55	0.45
CGGTGC	127	85	42	3.82E-03	2.42	0.45
GGACCG	107	65	42	1.32E-03	2.88	0.45
AGTCGG	108	66	42	1.42E-03	2.85	0.45
ATGAAC	352	310	42	1.02E-01	0.99	0.45
GTCGAG	86	44	42	2.30E-04	3.64	0.45
GTTGGC	296	254	42	7.34E-02	1.13	0.45
ACCTGC	445	403	42	1.51E-01	0.82	0.44
GAGCAT	363	321	42	1.10E-01	0.96	0.44
GCGAGA	100	58	42	9.41E-04	3.03	0.44
TGACGG	106	64	42	1.44E-03	2.84	0.44
TGTAGT	406	364	42	1.34E-01	0.87	0.44
CAGATG	584	542	42	2.15E-01	0.67	0.44
GCAAGC	327	285	42	9.30E-02	1.03	0.44
CCTCGG	181	139	42	2.04E-02	1.69	0.44
ACGGGG	133	92	41	5.71E-03	2.24	0.44
GGCATC	315	274	41	8.79E-02	1.06	0.44
TGGTAG	351	310	41	1.08E-01	0.97	0.44
AACGTG	143	102	41	8.69E-03	2.06	0.44
TGACAG	562	521	41	2.12E-01	0.67	0.44
TCCTGG	760	719	41	2.86E-01	0.54	0.43
AAGCGG	110	69	41	2.27E-03	2.64	0.43
AGACCG	106	65	41	1.80E-03	2.74	0.43
ACGGAC	96	55	41	9.02E-04	3.04	0.43
GACGGA	104	63	41	1.61E-03	2.79	0.43
TGTGCA	604	563	41	2.33E-01	0.63	0.43
ATGAAG	552	511	41	2.13E-01	0.67	0.43
CTGACG	123	83	40	4.79E-03	2.32	0.43
AAACTG	619	579	40	2.43E-01	0.61	0.43
TAGGGA	363	323	40	1.24E-01	0.91	0.43
GGCCGT	117	77	40	3.78E-03	2.42	0.43
GGACGC	103	63	40	1.78E-03	2.75	0.43
GAECTC	351	311	40	1.19E-01	0.92	0.43

GCCTGC	530	490	40	2.09E-01	0.68	0.42
AGTGGT	408	368	40	1.51E-01	0.82	0.42
AGGCCT	533	493	40	2.12E-01	0.67	0.42
TCCGTG	168	128	40	2.02E-02	1.69	0.42
AGTCAG	510	470	40	2.02E-01	0.69	0.42
ACCGGG	109	69	40	2.83E-03	2.55	0.42
GGATAG	248	208	40	6.26E-02	1.20	0.42
GCGTGC	122	82	40	5.41E-03	2.27	0.42
GACCGA	89	49	40	7.32E-04	3.14	0.42
CGAAGA	108	68	40	2.78E-03	2.56	0.42
GTGTCG	101	61	40	1.85E-03	2.73	0.42
GCCGCC	144	104	40	1.18E-02	1.93	0.42
GAGAAC	448	408	40	1.76E-01	0.75	0.42
ACCAGG	462	422	40	1.84E-01	0.74	0.42
TGAGAT	463	424	39	1.85E-01	0.73	0.42
CCGGAA	120	81	39	5.41E-03	2.27	0.42
GCCAGC	509	470	39	2.09E-01	0.68	0.42
TGGCAC	368	329	39	1.37E-01	0.86	0.42
TCTGGC	489	450	39	2.00E-01	0.70	0.42
ACCCCG	132	93	39	8.89E-03	2.05	0.42
CTCCCT	726	687	39	2.97E-01	0.53	0.42
GCATTG	336	297	39	1.19E-01	0.92	0.42
CTTCGG	124	85	39	6.81E-03	2.17	0.41
TGGCGT	124	85	39	6.81E-03	2.17	0.41
GGGTAC	206	167	39	4.32E-02	1.36	0.41
GCACCG	115	76	39	4.86E-03	2.31	0.41
AGGGTC	366	327	39	1.40E-01	0.85	0.41
GGGCGA	100	61	39	2.21E-03	2.66	0.41
ACGAGA	106	67	39	3.16E-03	2.50	0.41
TGTCCC	563	524	39	2.39E-01	0.62	0.41
GCCTCT	599	560	39	2.54E-01	0.59	0.41
AATGGA	487	448	39	2.06E-01	0.69	0.41
AGCGGA	106	67	39	3.34E-03	2.48	0.41
TCGGGC	108	69	39	3.77E-03	2.42	0.41
CACCGT	137	99	38	1.21E-02	1.92	0.41
AGACTT	525	487	38	2.26E-01	0.65	0.41
CACGGA	138	100	38	1.27E-02	1.89	0.41
TCGAGG	113	75	38	5.10E-03	2.29	0.41
ATTGTA	427	389	38	1.81E-01	0.74	0.41
TTGATG	426	388	38	1.80E-01	0.74	0.41
CACCGG	119	81	38	6.89E-03	2.16	0.40
GGATCT	313	275	38	1.15E-01	0.94	0.40
TCGAGA	96	58	38	2.11E-03	2.68	0.40
TCGGAC	79	41	38	4.99E-04	3.30	0.40
TCGTGG	133	95	38	1.16E-02	1.93	0.40
CGTCTG	148	110	38	1.78E-02	1.75	0.40
CCGTGC	147	109	38	1.74E-02	1.76	0.40
AGGATT	400	362	38	1.68E-01	0.77	0.40
GTTGCT	411	373	38	1.75E-01	0.76	0.40
AAGCAC	421	383	38	1.80E-01	0.74	0.40
ACGGGC	105	67	38	3.85E-03	2.41	0.40
CCTCTC	629	591	38	2.78E-01	0.56	0.40
CGAGAA	120	82	38	7.69E-03	2.11	0.40
TGACGT	128	90	38	1.04E-02	1.98	0.40

CCAGCC	684	646	38	3.00E-01	0.52	0.40
TAGACG	85	47	38	1.03E-03	2.99	0.40
GTGGTC	333	295	38	1.33E-01	0.88	0.40
GTGAAA	478	440	38	2.14E-01	0.67	0.40
CAGCGA	128	90	38	1.10E-02	1.96	0.40
ATCGGA	80	42	38	6.84E-04	3.16	0.40
TCGGAT	85	48	37	1.12E-03	2.95	0.40
GTCGGG	107	70	37	4.79E-03	2.32	0.40
CAGACG	131	94	37	1.24E-02	1.91	0.40
GCAGGA	124	87	37	9.82E-03	2.01	0.40
TTGTGA	539	502	37	2.46E-01	0.61	0.40
GGCACCA	412	375	37	1.83E-01	0.74	0.40
TTCGGG	110	73	37	5.76E-03	2.24	0.40
GCCACT	416	379	37	1.86E-01	0.73	0.40
GCCTCG	148	111	37	2.11E-02	1.68	0.39
GAGCGC	113	76	37	7.01E-03	2.15	0.39
GACACG	121	84	37	9.68E-03	2.01	0.39
CTTCTG	811	774	37	3.52E-01	0.45	0.39
GTCGGA	81	44	37	9.37E-04	3.03	0.39
TGATGT	507	470	37	2.37E-01	0.63	0.39
CTCGAG	122	85	37	1.02E-02	1.99	0.39
CACGTG	214	177	37	6.19E-02	1.21	0.39
ACGGGT	97	60	37	3.23E-03	2.49	0.39
GTCAGA	430	393	37	1.98E-01	0.70	0.39
TCTCGG	139	102	37	1.75E-02	1.76	0.39
TGCATG	486	449	37	2.28E-01	0.64	0.39
TCGGGA	124	87	37	1.13E-02	1.95	0.39
TATGGG	275	238	37	1.04E-01	0.98	0.39
TGCGGA	104	67	37	4.99E-03	2.30	0.39
ACTCGC	92	55	37	2.49E-03	2.60	0.39
CTCGTG	150	113	37	2.42E-02	1.62	0.39
CAGACC	404	367	37	1.88E-01	0.73	0.39
ATGTGA	522	485	37	2.50E-01	0.60	0.39
ACGTGT	169	133	36	3.59E-02	1.45	0.39
GGTGTC	344	308	36	1.54E-01	0.81	0.39
TGCCCT	609	573	36	2.91E-01	0.54	0.39
ACCGAG	125	89	36	1.30E-02	1.89	0.38
TGTGTA	637	601	36	3.03E-01	0.52	0.38
CGCCTG	153	117	36	2.75E-02	1.56	0.38
CGTTGG	104	68	36	5.86E-03	2.23	0.38
CTGTCG	124	88	36	1.32E-02	1.88	0.38
GAGTCG	97	61	36	4.16E-03	2.38	0.38
ATGGCA	420	384	36	2.06E-01	0.69	0.38
CGTGGC	155	119	36	3.09E-02	1.51	0.38
CCCTCG	142	106	36	2.37E-02	1.62	0.38
CCCTGA	529	493	36	2.65E-01	0.58	0.38
ACGTTG	110	74	36	8.81E-03	2.06	0.38
ACTCGG	128	93	35	1.68E-02	1.77	0.38
ATGGGT	342	307	35	1.64E-01	0.78	0.38
CGAGTG	119	84	35	1.30E-02	1.89	0.37
AGCCGC	127	92	35	1.70E-02	1.77	0.37
TGATGA	429	394	35	2.19E-01	0.66	0.37
TGCCGG	116	81	35	1.20E-02	1.92	0.37
GACGAA	80	45	35	1.62E-03	2.79	0.37

ACGGAA	115	80	35	1.18E-02	1.93	0.37
ACCGGA	93	58	35	4.27E-03	2.37	0.37
CTCGCA	95	60	35	4.92E-03	2.31	0.37
CAGTAG	370	335	35	1.88E-01	0.73	0.37
CGACTG	99	64	35	6.17E-03	2.21	0.37
AGGCCG	130	95	35	1.99E-02	1.70	0.37
TCAGGA	576	541	35	2.96E-01	0.53	0.37
AATCGG	78	43	35	1.56E-03	2.81	0.37
ACCCCT	388	353	35	2.02E-01	0.70	0.37
CGGAAA	111	76	35	1.11E-02	1.96	0.37
TAGAGC	301	266	35	1.45E-01	0.84	0.37
AGGTGT	434	399	35	2.29E-01	0.64	0.37
AACTCG	100	65	35	7.09E-03	2.15	0.37
GGGTCA	350	315	35	1.80E-01	0.74	0.37
ACTTTG	564	529	35	2.96E-01	0.53	0.37
AACGAA	105	70	35	9.09E-03	2.04	0.37
GTCTGC	419	384	35	2.23E-01	0.65	0.37
CGAGAC	91	56	35	4.49E-03	2.35	0.37
CCCTGC	647	613	34	3.31E-01	0.48	0.37
AGATGC	426	392	34	2.29E-01	0.64	0.36
AGTCTG	528	494	34	2.83E-01	0.55	0.36
GACCGG	89	55	34	4.53E-03	2.34	0.36
AACGGG	101	67	34	8.60E-03	2.07	0.36
GTTAGG	260	226	34	1.24E-01	0.91	0.36
CTGACT	539	505	34	2.94E-01	0.53	0.36
CGGTGA	115	81	34	1.55E-02	1.81	0.36
GGCGTC	97	63	34	7.46E-03	2.13	0.36
GCCAGA	463	429	34	2.57E-01	0.59	0.36
GTCTGA	418	384	34	2.33E-01	0.63	0.36
AAGGGT	381	347	34	2.11E-01	0.68	0.36
ACTGTC	453	419	34	2.54E-01	0.59	0.36
CCGGCC	132	98	34	2.65E-02	1.58	0.36
GGAGTT	367	333	34	2.03E-01	0.69	0.36
GCCCCG	137	103	34	3.03E-02	1.52	0.36
CGTAGG	85	51	34	4.03E-03	2.39	0.36
CGGCCA	120	87	33	2.00E-02	1.70	0.35
TTGAGA	512	479	33	2.89E-01	0.54	0.35
TAGGAT	293	260	33	1.55E-01	0.81	0.35
CCGCAG	145	112	33	3.73E-02	1.43	0.35
CCGCCT	149	116	33	4.04E-02	1.39	0.35
AGCACCA	566	533	33	3.14E-01	0.50	0.35
TGTCGT	117	84	33	1.90E-02	1.72	0.35
CTCCTG	798	765	33	4.01E-01	0.40	0.35
CGACAG	104	71	33	1.21E-02	1.92	0.35
GCTCCC	427	394	33	2.48E-01	0.61	0.35
CGGACT	91	58	33	6.67E-03	2.18	0.35
TTCTGA	729	696	33	3.83E-01	0.42	0.35
AGGCAT	387	354	33	2.27E-01	0.64	0.35
AGGCGT	106	73	33	1.41E-02	1.85	0.35
GC GG TG	125	92	33	2.58E-02	1.59	0.35
GCAAAG	451	418	33	2.66E-01	0.58	0.35
AGCGGC	114	81	33	1.90E-02	1.72	0.35
CGACCT	89	56	33	6.64E-03	2.18	0.35
CGGAGT	98	65	33	1.06E-02	1.97	0.35

ATCGTG	101	68	33	1.21E-02	1.92	0.35
CGAACT	74	41	33	2.41E-03	2.62	0.35
GCGCAG	119	86	33	2.32E-02	1.63	0.34
GGCGCA	89	56	33	7.03E-03	2.15	0.34
AGCGTG	141	109	32	4.02E-02	1.40	0.34
ACCCTG	540	508	32	3.17E-01	0.50	0.34
CGCTGC	159	127	32	5.54E-02	1.26	0.34
GGGATC	235	203	32	1.23E-01	0.91	0.34
CAGCCG	155	123	32	5.30E-02	1.28	0.34
CTGCGT	138	106	32	3.92E-02	1.41	0.34
GCGATG	92	60	32	9.00E-03	2.05	0.34
ACGTAG	89	57	32	7.73E-03	2.11	0.34
AGGCGA	101	69	32	1.36E-02	1.87	0.34
ATCAGG	330	298	32	2.00E-01	0.70	0.34
ACCGAC	75	43	32	3.16E-03	2.50	0.34
TTGTCG	87	55	32	7.14E-03	2.15	0.34
TCACGG	122	90	32	2.80E-02	1.55	0.34
GCTAGA	270	238	32	1.57E-01	0.80	0.34
AGGCAC	379	347	32	2.36E-01	0.63	0.34
GCGACT	79	47	32	4.54E-03	2.34	0.34
CAGTGA	609	577	32	3.56E-01	0.45	0.34
GTGGTA	302	270	32	1.85E-01	0.73	0.34
ATCGGG	83	51	32	6.31E-03	2.20	0.34
CCAGTG	609	577	32	3.58E-01	0.45	0.34
TGGAAA	768	736	32	4.14E-01	0.38	0.34
GAATCG	79	47	32	4.89E-03	2.31	0.34
AGCGGT	97	65	32	1.31E-02	1.88	0.34
GGGGCG	159	127	32	6.26E-02	1.20	0.33
GCCGGC	113	81	32	2.39E-02	1.62	0.33
CCAGCG	153	122	31	5.74E-02	1.24	0.33
TCGGTG	121	90	31	3.04E-02	1.52	0.33
GTGCGT	110	79	31	2.23E-02	1.65	0.33
TGCGGT	104	73	31	1.83E-02	1.74	0.33
GGTGTA	238	207	31	1.37E-01	0.86	0.33
GCGGAC	73	42	31	3.48E-03	2.46	0.33
CAGGCC	525	494	31	3.28E-01	0.48	0.33
TAGAAG	444	413	31	2.87E-01	0.54	0.33
GGCCCT	431	400	31	2.79E-01	0.55	0.33
CTGGCG	129	98	31	3.84E-02	1.42	0.33
CAAGGC	414	383	31	2.70E-01	0.57	0.33
TACGGG	71	40	31	3.13E-03	2.50	0.33
GCTCCT	538	507	31	3.36E-01	0.47	0.33
ACGCTG	140	109	31	4.89E-02	1.31	0.33
GGACTA	206	175	31	1.12E-01	0.95	0.33
AAGTAG	377	346	31	2.49E-01	0.60	0.33
CTCAGG	637	606	31	3.81E-01	0.42	0.33
ACCAGC	395	364	31	2.63E-01	0.58	0.33
CGGACC	77	46	31	5.46E-03	2.26	0.33
GCGGGC	117	86	31	3.09E-02	1.51	0.33
GAACGC	81	50	31	7.27E-03	2.14	0.33
CGCACT	90	59	31	1.20E-02	1.92	0.33
CTTGAG	482	451	31	3.16E-01	0.50	0.32
GTTTTG	706	675	31	4.10E-01	0.39	0.32
GACGTC	88	57	31	1.13E-02	1.95	0.32

TGCGCT	111	81	30	2.77E-02	1.56	0.32
GTATTG	281	251	30	1.87E-01	0.73	0.32
GTAGCC	255	225	30	1.65E-01	0.78	0.32
TAGGAA	492	462	30	3.25E-01	0.49	0.32
CTTGTG	555	525	30	3.55E-01	0.45	0.32
AAACGG	116	86	30	3.27E-02	1.48	0.32
CTCCCC	608	578	30	3.79E-01	0.42	0.32
GACGCC	89	59	30	1.28E-02	1.89	0.32
ACTCGA	84	54	30	1.02E-02	1.99	0.32
TGACGA	87	57	30	1.20E-02	1.92	0.32
AGACGA	100	70	30	2.12E-02	1.67	0.32
TCGGAA	99	69	30	2.05E-02	1.69	0.32
CAGGCA	593	563	30	3.78E-01	0.42	0.32
GACGCA	81	51	30	9.48E-03	2.02	0.32
GCGAGC	100	70	30	2.24E-02	1.65	0.32
GGCGGA	98	68	30	2.09E-02	1.68	0.32
TCGGGT	105	75	30	2.69E-02	1.57	0.32
CGACTC	82	52	30	1.06E-02	1.97	0.31
TACCTC	302	272	30	2.17E-01	0.66	0.31
ATGGCG	103	73	30	2.60E-02	1.58	0.31
CGGTAG	77	47	30	8.04E-03	2.09	0.31
CGTGGT	137	107	30	5.91E-02	1.23	0.31
GGGTCC	312	283	29	2.27E-01	0.64	0.31
CCCAAG	514	485	29	3.52E-01	0.45	0.31
GCTTGA	314	285	29	2.30E-01	0.64	0.31
ATAGAG	321	292	29	2.37E-01	0.62	0.31
CGGGAC	109	80	29	3.32E-02	1.48	0.31
AGACTC	393	364	29	2.90E-01	0.54	0.31
AAGCCG	117	88	29	4.24E-02	1.37	0.31
CTGCGC	123	94	29	4.85E-02	1.31	0.31
AGCGAA	84	55	29	1.37E-02	1.86	0.31
CGCTGT	147	118	29	7.47E-02	1.13	0.31
AACGCA	89	60	29	1.75E-02	1.76	0.31
TGCCCG	136	107	29	6.29E-02	1.20	0.31
CGTGCC	122	93	29	4.81E-02	1.32	0.31
ACGAAG	102	73	29	2.93E-02	1.53	0.31
CGTGCA	130	101	29	5.87E-02	1.23	0.30
TCACCG	110	81	29	3.76E-02	1.42	0.30
TGGCTC	522	493	29	3.68E-01	0.43	0.30
GAGATC	258	229	29	1.94E-01	0.71	0.30
AACCGG	81	52	29	1.31E-02	1.88	0.30
GCGGCC	111	82	29	3.99E-02	1.40	0.30
GTGCCG	101	72	29	3.01E-02	1.52	0.30
TGTCGA	75	46	29	9.55E-03	2.02	0.30
TGTTGC	392	363	29	2.99E-01	0.52	0.30
CACGGG	150	121	29	8.35E-02	1.08	0.30
CCATGG	496	468	28	3.59E-01	0.45	0.30
CGCAGG	125	97	28	5.60E-02	1.25	0.30
GATGCG	82	54	28	1.46E-02	1.83	0.30
CGGCCT	130	102	28	6.23E-02	1.21	0.30
TCAGAG	656	628	28	4.29E-01	0.37	0.30
CAAGCC	388	360	28	3.00E-01	0.52	0.30
ACACCG	106	78	28	3.74E-02	1.43	0.30
ACCGTT	91	63	28	2.30E-02	1.64	0.30

AGTGTA	371	343	28	2.92E-01	0.53	0.30
TGCCGC	110	82	28	4.25E-02	1.37	0.30
AAGGCT	522	494	28	3.79E-01	0.42	0.30
GAAAAG	665	637	28	4.38E-01	0.36	0.30
CCGTAG	81	53	28	1.55E-02	1.81	0.30
GCGGCT	119	91	28	5.33E-02	1.27	0.30
CGTGTG	136	108	28	7.35E-02	1.13	0.30
GTTAGA	290	262	28	2.35E-01	0.63	0.30
GTGGTT	419	391	28	3.27E-01	0.49	0.30
GC GGCA	94	66	28	2.80E-02	1.55	0.29
AATCGT	80	52	28	1.60E-02	1.79	0.29
CCAGCA	621	593	28	4.27E-01	0.37	0.29
TAGTGG	278	250	28	2.29E-01	0.64	0.29
AGTAGG	295	267	28	2.46E-01	0.61	0.29
GTTTGA	423	395	28	3.36E-01	0.47	0.29
TAGTGC	217	190	27	1.73E-01	0.76	0.29
ACAGAC	456	429	27	3.56E-01	0.45	0.29
TCGTGT	130	103	27	7.22E-02	1.14	0.29
CCCGTG	172	145	27	1.24E-01	0.91	0.29
ATTCTG	578	551	27	4.17E-01	0.38	0.29
GAGCTT	398	371	27	3.26E-01	0.49	0.29
GAGCCG	132	105	27	7.85E-02	1.11	0.29
CGAGCT	106	79	27	4.64E-02	1.33	0.29
CCCGCT	129	102	27	7.57E-02	1.12	0.29
ACGTGA	125	98	27	7.12E-02	1.15	0.29
CACTGC	514	487	27	3.95E-01	0.40	0.29
CGCATG	93	66	27	3.29E-02	1.48	0.29
CAAGCG	89	62	27	2.90E-02	1.54	0.28
GGTTGA	260	233	27	2.28E-01	0.64	0.28
GGATCG	71	44	27	1.27E-02	1.90	0.28
TCGTGA	99	72	27	4.16E-02	1.38	0.28
GAAGTA	347	320	27	3.03E-01	0.52	0.28
GCGGTA	63	36	27	7.61E-03	2.12	0.28
CGAGCA	106	79	27	5.08E-02	1.29	0.28
GCTCAG	582	555	27	4.31E-01	0.37	0.28
CCGGGA	139	112	27	9.42E-02	1.03	0.28
CGAAGG	104	78	26	4.96E-02	1.30	0.28
GAGGTA	270	244	26	2.43E-01	0.61	0.28
CCACCG	130	104	26	8.39E-02	1.08	0.28
GCTGAT	322	296	26	2.89E-01	0.54	0.28
GGTCGT	71	45	26	1.46E-02	1.84	0.28
TCGCAC	68	42	26	1.23E-02	1.91	0.28
CCTCGA	99	73	26	4.55E-02	1.34	0.28
ATGAGG	386	360	26	3.37E-01	0.47	0.28
ACGGCA	94	68	26	3.95E-02	1.40	0.28
CGATGC	88	62	26	3.28E-02	1.48	0.28
CTAGGG	307	281	26	2.83E-01	0.55	0.28
AGCATG	450	424	26	3.79E-01	0.42	0.28
GCCACC	408	382	26	3.55E-01	0.45	0.28
TCGGCT	106	80	26	5.68E-02	1.25	0.28
GTCCGG	78	52	26	2.34E-02	1.63	0.27
AGACGC	97	71	26	4.64E-02	1.33	0.27
GACGGT	85	59	26	3.22E-02	1.49	0.27
ACGACT	76	50	26	2.21E-02	1.66	0.27

CGGGCC	114	88	26	7.22E-02	1.14	0.27
TGCGAA	69	43	26	1.58E-02	1.80	0.27
CCGCTG	152	126	26	1.25E-01	0.90	0.27
GTATGG	244	218	26	2.35E-01	0.63	0.27
GATAGG	216	190	26	2.06E-01	0.69	0.27
TCCCGG	136	111	25	1.04E-01	0.98	0.27
CGTGT	148	123	25	1.21E-01	0.92	0.27
GACGAT	69	44	25	1.65E-02	1.78	0.27
CGAGGT	95	70	25	4.76E-02	1.32	0.27
CTCGTT	107	82	25	6.43E-02	1.19	0.27
CCTCGT	125	100	25	9.11E-02	1.04	0.27
TAGACT	322	297	25	3.09E-01	0.51	0.27
GAAAGC	479	454	25	4.07E-01	0.39	0.27
CCGGCA	95	70	25	4.90E-02	1.31	0.27
TGCCGT	119	94	25	8.33E-02	1.08	0.27
TTCCGT	123	98	25	8.92E-02	1.05	0.27
CACCAG	495	470	25	4.16E-01	0.38	0.27
GTTTAC	307	282	25	2.98E-01	0.53	0.27
CAGTCG	88	63	25	4.02E-02	1.40	0.27
GCGTGA	87	62	25	4.01E-02	1.40	0.27
GA ^c TTA	275	250	25	2.75E-01	0.56	0.27
ACAGCG	127	102	25	9.81E-02	1.01	0.27
CGTTCT	131	106	25	1.04E-01	0.98	0.27
ACGTGC	115	90	25	8.08E-02	1.09	0.27
CCC ^c GA	117	92	25	8.45E-02	1.07	0.26
TCGAAC	56	31	25	7.56E-03	2.12	0.26
TGTACT	402	377	25	3.72E-01	0.43	0.26
ATGGAA	554	529	25	4.49E-01	0.35	0.26
CTGTAT	483	458	25	4.17E-01	0.38	0.26
CACGGC	115	90	25	8.26E-02	1.08	0.26
GCTAGG	272	247	25	2.76E-01	0.56	0.26
TCGCAG	91	66	25	4.79E-02	1.32	0.26
AACGCT	95	70	25	5.41E-02	1.27	0.26
CCTGCT	730	705	25	5.13E-01	0.29	0.26
ACGACA	81	56	25	3.49E-02	1.46	0.26
CACCGC	109	84	25	7.57E-02	1.12	0.26
CGCAGT	93	68	25	5.20E-02	1.28	0.26
AGGATC	280	255	25	2.87E-01	0.54	0.26
AATGCG	67	42	25	1.85E-02	1.73	0.26
ACCAGA	441	416	25	4.00E-01	0.40	0.26
CAGCGT	144	119	25	1.29E-01	0.89	0.26
ACGGCC	89	64	25	4.78E-02	1.32	0.26
GCGAAG	81	57	24	3.69E-02	1.43	0.26
TGCGAG	84	60	24	4.12E-02	1.39	0.26
CCCCCG	129	105	24	1.10E-01	0.96	0.26
TGTGAT	507	483	24	4.38E-01	0.36	0.26
ACGCTC	87	63	24	4.60E-02	1.34	0.26
CCGAGA	119	95	24	9.49E-02	1.02	0.26
CCGGTG	112	88	24	8.41E-02	1.08	0.26
AACCCG	85	61	24	4.32E-02	1.36	0.26
GGCTAG	261	237	24	2.75E-01	0.56	0.26
CAGGGT	512	488	24	4.42E-01	0.35	0.26
GTCGCA	59	35	24	1.21E-02	1.92	0.26
TACCCC	232	208	24	2.47E-01	0.61	0.26

TGCGGG	109	85	24	8.15E-02	1.09	0.26
AGAGTT	481	457	24	4.28E-01	0.37	0.26
CACGGT	121	97	24	1.01E-01	1.00	0.26
ACGACC	60	36	24	1.34E-02	1.87	0.26
CGAACC	60	36	24	1.34E-02	1.87	0.26
TGGAAT	480	456	24	4.31E-01	0.37	0.26
TTCGGA	84	60	24	4.47E-02	1.35	0.26
CCCGGT	97	73	24	6.55E-02	1.18	0.25
GTTGAT	280	256	24	3.00E-01	0.52	0.25
CGGCCG	67	43	24	2.24E-02	1.65	0.25
GCAACA	288	264	24	3.09E-01	0.51	0.25
GTCGTG	88	64	24	5.30E-02	1.28	0.25
GGAATT	377	353	24	3.78E-01	0.42	0.25
CGGATT	69	45	24	2.60E-02	1.59	0.25
AACCAG	421	397	24	4.06E-01	0.39	0.25
ACCGAA	79	55	24	4.04E-02	1.39	0.25
GTAGGT	249	225	24	2.76E-01	0.56	0.25
ACGATG	92	68	24	6.11E-02	1.21	0.25
ACCTCA	445	421	24	4.22E-01	0.37	0.25
GATCGT	67	43	24	2.46E-02	1.61	0.25
CCGGCT	124	100	24	1.15E-01	0.94	0.25
TTAGGG	306	282	24	3.31E-01	0.48	0.25
ACACGG	127	104	23	1.22E-01	0.91	0.25
CCCTTG	471	448	23	4.39E-01	0.36	0.25
AACGAC	66	43	23	2.47E-02	1.61	0.25
CCTTAG	354	331	23	3.71E-01	0.43	0.25
CCGCCA	113	90	23	1.01E-01	1.00	0.25
TGTACG	80	57	23	4.62E-02	1.34	0.25
TCGGTC	79	56	23	4.50E-02	1.35	0.25
TGATCG	67	44	23	2.75E-02	1.56	0.25
GCACAA	299	276	23	3.35E-01	0.48	0.25
CCCAGC	681	658	23	5.28E-01	0.28	0.24
GCATCG	84	61	23	5.55E-02	1.26	0.24
GCCGCT	114	91	23	1.08E-01	0.97	0.24
CGGAAC	75	52	23	4.09E-02	1.39	0.24
CTAGGA	351	328	23	3.79E-01	0.42	0.24
ATGCGA	61	38	23	2.12E-02	1.67	0.24
GGCTCA	407	384	23	4.15E-01	0.38	0.24
GGTTGC	226	203	23	2.69E-01	0.57	0.24
CCCTGT	593	570	23	5.03E-01	0.30	0.24
TGCTAG	315	292	23	3.54E-01	0.45	0.24
GAGATT	340	317	23	3.73E-01	0.43	0.24
GACACC	294	271	23	3.37E-01	0.47	0.24
GAAACG	115	92	23	1.13E-01	0.95	0.24
ACGAGG	102	79	23	9.02E-02	1.04	0.24
CTCCTC	646	623	23	5.23E-01	0.28	0.24
ACTTCG	79	56	23	5.16E-02	1.29	0.24
GCATGA	290	267	23	3.37E-01	0.47	0.24
CACAGG	630	607	23	5.20E-01	0.28	0.24
GACTAG	211	188	23	2.57E-01	0.59	0.24
GACGCT	94	71	23	7.85E-02	1.11	0.24
TGTTAG	380	357	23	4.06E-01	0.39	0.24
CCGTGA	123	100	23	1.32E-01	0.88	0.24
CACTCG	105	82	23	1.00E-01	1.00	0.24

CCCAGA	650	627	23	5.29E-01	0.28	0.24
GGCGAC	70	48	22	3.80E-02	1.42	0.24
AGATCG	69	47	22	3.67E-02	1.44	0.24
GGTAGC	221	199	22	2.73E-01	0.56	0.24
AGCCTT	574	552	22	5.04E-01	0.30	0.24
GCGAAC	50	28	22	1.10E-02	1.96	0.24
GCGTCC	88	66	22	7.09E-02	1.15	0.24
AACGAG	86	64	22	6.83E-02	1.17	0.24
CGGCAA	67	45	22	3.51E-02	1.45	0.24
GAGGTT	335	313	22	3.83E-01	0.42	0.24
GGCCTT	450	428	22	4.54E-01	0.34	0.24
TGCACG	116	94	22	1.25E-01	0.90	0.24
TGCGTT	102	80	22	1.00E-01	1.00	0.23
CGTGAA	107	85	22	1.10E-01	0.96	0.23
GGTGAT	292	270	22	3.50E-01	0.46	0.23
CGAATG	80	58	22	6.02E-02	1.22	0.23
CCTTGC	447	425	22	4.55E-01	0.34	0.23
CATGTG	571	549	22	5.11E-01	0.29	0.23
CCGACT	86	64	22	7.25E-02	1.14	0.23
GGTTTT	667	645	22	5.44E-01	0.26	0.23
CTGACA	496	474	22	4.81E-01	0.32	0.23
GTTCGG	67	45	22	3.86E-02	1.41	0.23
AGCGTC	95	73	22	9.16E-02	1.04	0.23
CCGAGT	115	93	22	1.33E-01	0.88	0.23
AAGACC	342	320	22	4.02E-01	0.40	0.23
AGGGTA	285	263	22	3.57E-01	0.45	0.23
CTACGA	57	36	21	2.56E-02	1.59	0.23
ATGCAA	356	335	21	4.15E-01	0.38	0.23
GGGTCG	80	59	21	6.88E-02	1.16	0.23
ACTGCG	91	70	21	9.11E-02	1.04	0.23
CGCCAT	97	76	21	1.03E-01	0.99	0.23
CCCGGC	125	104	21	1.57E-01	0.80	0.23
ACCTCG	97	76	21	1.04E-01	0.98	0.23
GCCGAC	67	46	21	4.43E-02	1.35	0.23
ACGCAC	86	65	21	8.20E-02	1.09	0.23
GCGGGT	87	66	21	8.45E-02	1.07	0.23
ACCGCC	87	66	21	8.50E-02	1.07	0.23
GAACTA	253	232	21	3.35E-01	0.48	0.23
CGTCCT	124	103	21	1.58E-01	0.80	0.23
GCCCCC	325	304	21	3.97E-01	0.40	0.22
TGGGTA	353	332	21	4.18E-01	0.38	0.22
ACCTCC	389	368	21	4.41E-01	0.36	0.22
ATCTGA	423	402	21	4.61E-01	0.34	0.22
CGTTTG	127	106	21	1.66E-01	0.78	0.22
GCGGCG	69	48	21	5.04E-02	1.30	0.22
AAAGCG	99	78	21	1.12E-01	0.95	0.22
GACCCA	354	333	21	4.20E-01	0.38	0.22
ACTGCC	425	404	21	4.64E-01	0.33	0.22
GTGTAC	261	240	21	3.48E-01	0.46	0.22
CAGCCA	660	639	21	5.61E-01	0.25	0.22
GATGAT	293	272	21	3.78E-01	0.42	0.22
CCAGAA	605	584	21	5.44E-01	0.26	0.22
AAAGGC	467	446	21	4.90E-01	0.31	0.22
TCGCTG	125	104	21	1.69E-01	0.77	0.22

ATAGGA	315	294	21	3.99E-01	0.40	0.22
TCCGAG	115	94	21	1.51E-01	0.82	0.22
AAACGC	87	66	21	9.34E-02	1.03	0.22
GCAACG	63	42	21	4.32E-02	1.36	0.22
ATCTGG	390	369	21	4.52E-01	0.35	0.22
ATTTGG	471	450	21	4.95E-01	0.31	0.22
CCAGGC	598	577	21	5.45E-01	0.26	0.22
TGACCC	351	330	21	4.28E-01	0.37	0.22
AGCACG	115	94	21	1.54E-01	0.81	0.22
ACGGAT	73	52	21	6.59E-02	1.18	0.22
TACTCG	65	44	21	4.91E-02	1.31	0.22
AAGCGT	90	69	21	1.04E-01	0.98	0.22
TTGACG	68	48	20	5.65E-02	1.25	0.22
TCGTCC	85	65	20	9.45E-02	1.02	0.22
GCCTTC	481	461	20	5.07E-01	0.30	0.22
TCGTTTC	85	65	20	9.62E-02	1.02	0.22
GCCAGT	397	377	20	4.65E-01	0.33	0.22
CATGGA	467	447	20	5.01E-01	0.30	0.22
TTGCGG	70	50	20	6.40E-02	1.19	0.21
TCGGCA	78	58	20	8.23E-02	1.08	0.21
CAGTGT	702	682	20	5.87E-01	0.23	0.21
TGCCGA	86	66	20	1.01E-01	0.99	0.21
TCCCCG	149	129	20	2.26E-01	0.65	0.21
GCGTTT	104	84	20	1.41E-01	0.85	0.21
ACGAAC	62	42	20	4.84E-02	1.32	0.21
GTGCAC	309	289	20	4.11E-01	0.39	0.21
GCGTCA	73	53	20	7.36E-02	1.13	0.21
GCCGGT	78	58	20	8.52E-02	1.07	0.21
GCGCCT	102	82	20	1.40E-01	0.85	0.21
GTCGGC	66	46	20	5.87E-02	1.23	0.21
GCATGT	382	362	20	4.65E-01	0.33	0.21
ACCGCT	83	63	20	9.92E-02	1.00	0.21
CCTGAC	424	404	20	4.89E-01	0.31	0.21
TTGCGA	55	35	20	3.63E-02	1.44	0.21
ATTGAG	301	281	20	4.11E-01	0.39	0.21
CACCGA	95	75	20	1.28E-01	0.89	0.21
TCCCTG	743	723	20	6.05E-01	0.22	0.21
CTCTCG	120	100	20	1.83E-01	0.74	0.21
CGTGAC	100	80	20	1.41E-01	0.85	0.21
GTCTCG	87	67	20	1.14E-01	0.94	0.21
TAGGCA	297	277	20	4.14E-01	0.38	0.21
GC GGAT	60	40	20	5.14E-02	1.29	0.21
TGACGC	72	53	19	8.13E-02	1.09	0.21
ACTGCT	509	490	19	5.39E-01	0.27	0.21
AAGCGA	84	65	19	1.11E-01	0.95	0.21
AAGTGC	349	330	19	4.57E-01	0.34	0.21
AAAACG	129	110	19	2.10E-01	0.68	0.21
CAAGTG	436	417	19	5.09E-01	0.29	0.20
GCTTGT	403	384	19	4.92E-01	0.31	0.20
TAGAGT	328	309	19	4.46E-01	0.35	0.20
CGTTAG	70	51	19	8.00E-02	1.10	0.20
CGATGG	86	67	19	1.20E-01	0.92	0.20
GGCCCG	105	86	19	1.64E-01	0.78	0.20
CGTCAG	104	85	19	1.62E-01	0.79	0.20

TGGTCG	71	52	19	8.30E-02	1.08	0.20
GAGGTC	299	280	19	4.26E-01	0.37	0.20
AAATCG	81	62	19	1.10E-01	0.96	0.20
CGTCCA	88	69	19	1.28E-01	0.89	0.20
CTCGAA	78	59	19	1.04E-01	0.98	0.20
ATGCGG	69	50	19	8.17E-02	1.09	0.20
GCTCGG	111	92	19	1.83E-01	0.74	0.20
CCCGTT	98	79	19	1.54E-01	0.81	0.20
GCTTCG	94	75	19	1.45E-01	0.84	0.20
CCGTTG	85	66	19	1.23E-01	0.91	0.20
ACGAGC	71	52	19	8.78E-02	1.06	0.20
TTTGAG	570	551	19	5.73E-01	0.24	0.20
ACTCGT	83	64	19	1.20E-01	0.92	0.20
AGCCCT	549	530	19	5.68E-01	0.25	0.20
CCCCGA	119	100	19	2.06E-01	0.69	0.20
GGCGGT	86	67	19	1.30E-01	0.89	0.20
AACCGC	64	45	19	7.44E-02	1.13	0.20
ACGCCA	88	69	19	1.38E-01	0.86	0.20
GGGCGC	98	79	19	1.63E-01	0.79	0.20
CGCTCT	120	101	19	2.12E-01	0.67	0.20
CCCCGC	157	138	19	2.80E-01	0.55	0.20
TCCTCG	130	112	18	2.34E-01	0.63	0.20
TGTTCG	83	65	18	1.30E-01	0.89	0.20
TGCAAG	362	344	18	4.89E-01	0.31	0.19
AGCGCC	104	86	18	1.83E-01	0.74	0.19
ACAGTG	625	607	18	6.02E-01	0.22	0.19
GGTCCC	317	299	18	4.61E-01	0.34	0.19
ACACGA	91	73	18	1.53E-01	0.82	0.19
ATCACG	76	58	18	1.14E-01	0.94	0.19
TAGCTG	394	376	18	5.10E-01	0.29	0.19
GTCGTT	73	55	18	1.06E-01	0.97	0.19
TACGGA	65	47	18	8.43E-02	1.07	0.19
GCCCGT	96	78	18	1.68E-01	0.77	0.19
AACCGA	77	59	18	1.20E-01	0.92	0.19
TTACCG	62	44	18	7.80E-02	1.11	0.19
TCACGC	80	62	18	1.28E-01	0.89	0.19
TTGTTG	535	517	18	5.76E-01	0.24	0.19
CGCCTC	125	107	18	2.36E-01	0.63	0.19
GTGCAA	264	246	18	4.25E-01	0.37	0.19
GAGCGT	88	70	18	1.52E-01	0.82	0.19
GCTTCT	602	584	18	6.02E-01	0.22	0.19
GGCCGC	101	83	18	1.85E-01	0.73	0.19
GCGCAT	66	48	18	9.28E-02	1.03	0.19
AAGGCG	96	78	18	1.74E-01	0.76	0.19
GCGTCT	98	80	18	1.80E-01	0.74	0.19
CCGAAG	100	82	18	1.86E-01	0.73	0.19
CCGACA	73	55	18	1.15E-01	0.94	0.19
TAGGGT	251	233	18	4.17E-01	0.38	0.19
CCGGAT	68	50	18	1.02E-01	0.99	0.19
GCCGCA	86	68	18	1.53E-01	0.82	0.19
CGGCAT	69	51	18	1.06E-01	0.97	0.19
TGGCGA	85	67	18	1.51E-01	0.82	0.19
CGTAGC	67	49	18	1.01E-01	0.99	0.19
TCGAGC	67	49	18	1.01E-01	0.99	0.19

CCTCGC	110	92	18	2.14E-01	0.67	0.19
TGCTTG	532	514	18	5.85E-01	0.23	0.19
GGCTAC	212	194	18	3.83E-01	0.42	0.19
TCGTAG	64	46	18	9.40E-02	1.03	0.19
CGCAGC	120	102	18	2.38E-01	0.62	0.19
ACCGTA	61	43	18	8.54E-02	1.07	0.19
CAAAGG	518	500	18	5.83E-01	0.23	0.19
TTAACG	71	54	17	1.18E-01	0.93	0.18
CGCCTT	108	91	17	2.16E-01	0.66	0.18
AACGCG	31	14	17	9.09E-03	2.04	0.18
TGAATC	291	274	17	4.64E-01	0.33	0.18
CGCACCA	104	87	17	2.08E-01	0.68	0.18
CTTCCG	129	112	17	2.62E-01	0.58	0.18
GGCTCG	93	76	17	1.81E-01	0.74	0.18
GCCATG	420	403	17	5.45E-01	0.26	0.18
GACCCG	85	68	17	1.60E-01	0.80	0.18
TTGCCG	81	64	17	1.49E-01	0.83	0.18
TAAACG	88	71	17	1.70E-01	0.77	0.18
CGCGTG	52	35	17	6.39E-02	1.19	0.18
GTCCCC	372	355	17	5.22E-01	0.28	0.18
GTCAGC	354	337	17	5.16E-01	0.29	0.18
ACCGGC	70	53	17	1.24E-01	0.91	0.18
CGGAAT	66	49	17	1.12E-01	0.95	0.18
GTGCGG	90	73	17	1.83E-01	0.74	0.18
TCGCCT	101	84	17	2.12E-01	0.67	0.18
TCTCGT	100	83	17	2.11E-01	0.68	0.18
GCTCCG	123	106	17	2.64E-01	0.58	0.18
GCCGTC	81	64	17	1.61E-01	0.79	0.18
GATCAG	266	249	17	4.57E-01	0.34	0.18
TTCGAG	76	59	17	1.47E-01	0.83	0.18
CGCGCT	48	31	17	5.81E-02	1.24	0.18
CGGATC	58	41	17	9.08E-02	1.04	0.18
TCTGTC	654	637	17	6.39E-01	0.19	0.18
CTCCGT	133	116	17	2.87E-01	0.54	0.18
GCCACG	126	109	17	2.73E-01	0.56	0.18
ACGATT	68	51	17	1.25E-01	0.90	0.18
ATGACG	80	63	17	1.62E-01	0.79	0.18
CGTTGT	95	78	17	2.04E-01	0.69	0.18
GCGAGT	69	52	17	1.29E-01	0.89	0.18
GTAACG	58	41	17	9.37E-02	1.03	0.18
GCACTT	363	346	17	5.31E-01	0.28	0.18
CTCCGG	121	104	17	2.67E-01	0.57	0.18
ATTCGG	68	51	17	1.27E-01	0.89	0.18
ACCACG	107	90	17	2.37E-01	0.63	0.18
GCGGAA	68	51	17	1.28E-01	0.89	0.18
ATAACG	60	43	17	1.02E-01	0.99	0.18
TGGGTC	377	360	17	5.41E-01	0.27	0.18
AAGTCG	73	56	17	1.46E-01	0.84	0.18
TACGCA	59	42	17	1.01E-01	0.99	0.17
TAACGA	59	43	16	1.02E-01	0.99	0.17
AGCTCT	591	575	16	6.30E-01	0.20	0.17
AGTTGA	356	340	16	5.34E-01	0.27	0.17
GGAGTA	225	209	16	4.31E-01	0.37	0.17
TGACCA	399	383	16	5.58E-01	0.25	0.17

CCTGCA	559	543	16	6.23E-01	0.21	0.17
CCACGC	115	99	16	2.67E-01	0.57	0.17
GCCCCG	149	133	16	3.35E-01	0.48	0.17
AGTGCT	488	472	16	6.02E-01	0.22	0.17
CCTGTC	563	547	16	6.29E-01	0.20	0.17
CTTTCG	86	70	16	1.98E-01	0.70	0.17
CTCCGA	101	85	16	2.39E-01	0.62	0.17
CGGCCG	54	38	16	9.46E-02	1.02	0.17
ACTACG	51	35	16	8.49E-02	1.07	0.17
CCACGG	143	127	16	3.31E-01	0.48	0.17
CCGGTC	71	55	16	1.56E-01	0.81	0.17
CTTGC G	72	56	16	1.60E-01	0.79	0.17
GTCACG	93	77	16	2.24E-01	0.65	0.17
TCGTCT	98	82	16	2.37E-01	0.62	0.17
CGAGCC	95	79	16	2.30E-01	0.64	0.17
CGGTCA	77	61	16	1.79E-01	0.75	0.17
AAGCGC	75	59	16	1.74E-01	0.76	0.17
GTCCCG	97	81	16	2.38E-01	0.62	0.17
CCGCTT	90	74	16	2.22E-01	0.65	0.17
CCGACG	33	17	16	2.79E-02	1.55	0.17
CTCACG	114	98	16	2.84E-01	0.55	0.17
TCCGGG	110	94	16	2.77E-01	0.56	0.16
ACGAAA	77	61	16	1.87E-01	0.73	0.16
CATCGG	77	61	16	1.88E-01	0.73	0.16
CGCTCA	98	83	15	2.49E-01	0.60	0.16
TTGCGT	72	57	15	1.72E-01	0.76	0.16
CGGTGT	107	92	15	2.74E-01	0.56	0.16
AGCGAC	67	52	15	1.58E-01	0.80	0.16
CGGTTT	99	84	15	2.55E-01	0.59	0.16
CCGGAC	65	50	15	1.53E-01	0.82	0.16
CACACG	146	131	15	3.59E-01	0.44	0.16
ATCGTC	62	47	15	1.44E-01	0.84	0.16
GCTAGT	195	180	15	4.31E-01	0.37	0.16
GCGCGC	66	51	15	1.58E-01	0.80	0.16
GGTCGC	56	41	15	1.22E-01	0.91	0.16
AGGAAT	461	446	15	6.15E-01	0.21	0.16
TGTCAG	536	521	15	6.42E-01	0.19	0.16
ATGTCG	67	52	15	1.66E-01	0.78	0.16
TTCTGT	947	932	15	7.28E-01	0.14	0.16
GAAC TT	406	391	15	5.94E-01	0.23	0.16
CTGCAA	383	368	15	5.83E-01	0.23	0.16
ACTCCG	83	68	15	2.22E-01	0.65	0.16
ATCGCC	62	47	15	1.50E-01	0.82	0.16
TAACGC	49	34	15	9.94E-02	1.00	0.16
CGACAA	55	40	15	1.25E-01	0.90	0.16
TCTGAA	655	640	15	6.79E-01	0.17	0.16
AGCCCC	119	104	15	3.19E-01	0.50	0.16
TGCGTC	74	59	15	1.97E-01	0.70	0.16
GCCCCG	83	68	15	2.27E-01	0.64	0.16
TTCGGT	82	67	15	2.24E-01	0.65	0.16
TGCGAC	50	35	15	1.09E-01	0.96	0.16
GTCGTA	46	31	15	9.24E-02	1.03	0.16
TTTGCG	70	55	15	1.87E-01	0.73	0.16
AACGTT	106	91	15	2.95E-01	0.53	0.16

GGAAAC	439	424	15	6.17E-01	0.21	0.16
TGCGCA	87	72	15	2.48E-01	0.61	0.15
GGCGTA	45	30	15	9.32E-02	1.03	0.15
CGGTCT	82	67	15	2.33E-01	0.63	0.15
GTCGCC	69	54	15	1.90E-01	0.72	0.15
ATCTCG	69	54	15	1.90E-01	0.72	0.15
CCGGGT	98	83	15	2.80E-01	0.55	0.15
AGTCGA	56	41	15	1.41E-01	0.85	0.15
ATGCGC	63	48	15	1.70E-01	0.77	0.15
GGCGAT	60	46	14	1.58E-01	0.80	0.15
CCTGCG	130	116	14	3.56E-01	0.45	0.15
GATCCG	59	45	14	1.56E-01	0.81	0.15
GCCCTC	408	394	14	6.10E-01	0.21	0.15
CCTTCG	96	82	14	2.80E-01	0.55	0.15
CTTCGT	103	89	14	2.99E-01	0.52	0.15
CCTGTA	390	376	14	6.04E-01	0.22	0.15
AGAGTC	389	375	14	6.03E-01	0.22	0.15
CCGAAC	52	38	14	1.30E-01	0.89	0.15
TTCGGC	57	43	14	1.52E-01	0.82	0.15
ACGGCT	89	75	14	2.64E-01	0.58	0.15
CTTAGG	334	320	14	5.79E-01	0.24	0.15
CGGACG	32	18	14	4.48E-02	1.35	0.15
CGAGGC	114	100	14	3.33E-01	0.48	0.15
CGTCCC	101	87	14	3.02E-01	0.52	0.15
CGTTTA	86	72	14	2.60E-01	0.58	0.15
CAAGAC	322	308	14	5.74E-01	0.24	0.15
TCGTCG	30	16	14	3.82E-02	1.42	0.15
ATTGCG	46	32	14	1.12E-01	0.95	0.15
ATCGGC	49	35	14	1.26E-01	0.90	0.15
AACCCT	378	364	14	6.08E-01	0.22	0.15
GTCCCT	462	448	14	6.44E-01	0.19	0.15
CATGCG	80	66	14	2.55E-01	0.59	0.15
TACCGA	55	41	14	1.61E-01	0.79	0.15
GTCGGT	64	50	14	2.01E-01	0.70	0.15
GGTCCG	61	47	14	1.89E-01	0.72	0.14
ATCGGT	53	39	14	1.55E-01	0.81	0.14
CGCGGA	36	22	14	7.42E-02	1.13	0.14
GGTTAG	225	211	14	5.15E-01	0.29	0.14
TGCAAT	294	280	14	5.72E-01	0.24	0.14
AGCGCA	81	67	14	2.67E-01	0.57	0.14
GTTGCG	48	34	14	1.36E-01	0.87	0.14
CGACCG	29	16	13	4.30E-02	1.37	0.14
ATAGGG	198	185	13	4.91E-01	0.31	0.14
TCCGGC	74	61	13	2.46E-01	0.61	0.14
TCCGGA	82	69	13	2.75E-01	0.56	0.14
AGGTCTG	64	51	13	2.12E-01	0.67	0.14
AGCGCT	107	94	13	3.45E-01	0.46	0.14
ACCGGT	55	42	13	1.78E-01	0.75	0.14
CGTGAT	80	67	13	2.74E-01	0.56	0.14
GCGTTG	72	59	13	2.47E-01	0.61	0.14
TTTTGG	592	579	13	7.01E-01	0.15	0.14
AGCCGA	91	78	13	3.12E-01	0.51	0.14
CTCCCCG	142	129	13	4.26E-01	0.37	0.14
GCGCTT	82	69	13	2.86E-01	0.54	0.14

GATACT	238	225	13	5.43E-01	0.26	0.14
GTGCGA	54	41	13	1.81E-01	0.74	0.14
GCGACA	59	46	13	2.03E-01	0.69	0.14
AACGAT	65	52	13	2.28E-01	0.64	0.14
CGCAAC	40	27	13	1.12E-01	0.95	0.14
GTACGG	48	35	13	1.54E-01	0.81	0.14
TAGCGG	49	36	13	1.61E-01	0.79	0.14
TGCTCG	98	85	13	3.40E-01	0.47	0.14
CGCTAG	52	39	13	1.77E-01	0.75	0.14
GGCAA	356	343	13	6.26E-01	0.20	0.14
AAGGAT	400	387	13	6.46E-01	0.19	0.14
CGGGCG	54	41	13	1.88E-01	0.73	0.14
CGCACCC	72	59	13	2.62E-01	0.58	0.14
AGCTAG	307	294	13	6.01E-01	0.22	0.14
TGGCAA	375	362	13	6.37E-01	0.20	0.14
TCGTTT	126	113	13	4.09E-01	0.39	0.14
CGGGAT	73	60	13	2.68E-01	0.57	0.14
CAAACG	88	75	13	3.20E-01	0.50	0.13
CACGCA	106	93	13	3.69E-01	0.43	0.13
TGTATG	484	471	13	6.82E-01	0.17	0.13
GCATTG	290	277	13	5.96E-01	0.22	0.13
ATACGG	51	38	13	1.82E-01	0.74	0.13
AGCACC	346	333	13	6.28E-01	0.20	0.13
CGTCGC	29	16	13	6.14E-02	1.21	0.13
GCTCGT	73	60	13	2.75E-01	0.56	0.13
CGCTGA	104	91	13	3.68E-01	0.43	0.13
TCGCCG	35	22	13	9.72E-02	1.01	0.13
CTGTTA	417	404	13	6.61E-01	0.18	0.13
CGTTGC	71	58	13	2.71E-01	0.57	0.13
ACTTGC	304	292	12	6.10E-01	0.22	0.13
CGGTTG	73	61	12	2.81E-01	0.55	0.13
ACCGCG	34	22	12	9.55E-02	1.02	0.13
GGCAAC	200	188	12	5.33E-01	0.27	0.13
AGCAAC	296	284	12	6.10E-01	0.21	0.13
GTATGA	248	236	12	5.77E-01	0.24	0.13
CGTACT	54	42	12	2.10E-01	0.68	0.13
CGCCAA	65	53	12	2.59E-01	0.59	0.13
AGCCCC	456	444	12	6.83E-01	0.17	0.13
CTGATC	275	263	12	5.98E-01	0.22	0.13
TTGGCC	343	331	12	6.38E-01	0.20	0.13
ACGGTT	78	66	12	3.08E-01	0.51	0.13
CTCGTC	82	70	12	3.23E-01	0.49	0.13
CCGTCT	114	102	12	4.09E-01	0.39	0.13
GATAGA	257	245	12	5.89E-01	0.23	0.13
AACGTA	68	56	12	2.77E-01	0.56	0.13
TGCGGC	83	71	12	3.31E-01	0.48	0.13
CCGTTA	57	45	12	2.32E-01	0.63	0.13
CAACGA	55	43	12	2.23E-01	0.65	0.13
CGTATG	61	49	12	2.50E-01	0.60	0.13
AAACCG	86	74	12	3.41E-01	0.47	0.13
CTCGGT	110	98	12	4.04E-01	0.39	0.13
CGAGAT	64	52	12	2.64E-01	0.58	0.13
GACGTA	52	40	12	2.11E-01	0.68	0.13
CGCAAG	62	50	12	2.57E-01	0.59	0.13

GTCGAA	42	30	12	1.58E-01	0.80	0.13
CGAACCA	62	50	12	2.60E-01	0.59	0.13
GGATTC	275	263	12	6.08E-01	0.22	0.13
GTTACG	49	37	12	2.02E-01	0.70	0.13
ACCGCA	74	62	12	3.10E-01	0.51	0.13
AAGCCA	598	586	12	7.31E-01	0.14	0.13
CCTACG	59	47	12	2.51E-01	0.60	0.13
CGACGG	29	17	12	8.21E-02	1.09	0.13
TCTGCG	108	96	12	4.09E-01	0.39	0.13
ACGCGG	34	22	12	1.16E-01	0.93	0.12
CGTGTAA	95	83	12	3.78E-01	0.42	0.12
ACGTCA	90	78	12	3.66E-01	0.44	0.12
AAACGA	97	85	12	3.86E-01	0.41	0.12
CGTTGA	68	56	12	2.95E-01	0.53	0.12
TTTCGG	73	61	12	3.14E-01	0.50	0.12
GCGAAT	43	31	12	1.77E-01	0.75	0.12
ACAGGC	407	395	12	6.81E-01	0.17	0.12
GTCGAC	35	23	12	1.30E-01	0.89	0.12
AGGCAA	407	395	12	6.83E-01	0.17	0.12
TCCGAC	54	42	12	2.39E-01	0.62	0.12
TGTCGC	71	59	12	3.11E-01	0.51	0.12
CCGTTTC	89	77	12	3.70E-01	0.43	0.12
ACCCGT	76	64	12	3.30E-01	0.48	0.12
CGAACG	23	11	12	4.92E-02	1.31	0.12
CGGCTC	109	97	12	4.23E-01	0.37	0.12
GTTTCG	62	50	12	2.78E-01	0.56	0.12
CGTCTT	106	94	12	4.16E-01	0.38	0.12
GATTAG	53	42	11	2.37E-01	0.63	0.12
CGACTA	37	26	11	1.46E-01	0.83	0.12
AATTGG	272	261	11	6.20E-01	0.21	0.12
TAGTGT	355	344	11	6.65E-01	0.18	0.12
GGATTA	202	191	11	5.65E-01	0.25	0.12
CAGCCT	715	704	11	7.62E-01	0.12	0.12
GACCTT	348	337	11	6.63E-01	0.18	0.12
CTGTCA	583	572	11	7.38E-01	0.13	0.12
GCTAAG	287	276	11	6.31E-01	0.20	0.12
TTGACC	254	243	11	6.11E-01	0.21	0.12
CGCCAG	102	91	11	4.15E-01	0.38	0.12
GCCATC	321	310	11	6.53E-01	0.18	0.12
GCTACG	51	40	11	2.36E-01	0.63	0.12
CCGGTT	69	58	11	3.17E-01	0.50	0.12
GCACGT	97	86	11	4.05E-01	0.39	0.12
GTGCTC	374	363	11	6.79E-01	0.17	0.12
ACGCCT	83	72	11	3.67E-01	0.43	0.12
CCGATG	76	65	11	3.45E-01	0.46	0.12
GGATCC	233	222	11	6.01E-01	0.22	0.12
TGGTCC	342	331	11	6.67E-01	0.18	0.12
CCCGAT	59	48	11	2.82E-01	0.55	0.12
ACCCGG	91	80	11	3.95E-01	0.40	0.12
ACTCCC	315	304	11	6.58E-01	0.18	0.12
GCAGTA	271	260	11	6.36E-01	0.20	0.12
ACGCTA	50	39	11	2.48E-01	0.61	0.12
CCCCGT	114	103	11	4.59E-01	0.34	0.12
CAGGCT	620	609	11	7.56E-01	0.12	0.12

CACGAC	57	46	11	2.85E-01	0.55	0.12
CCCGCA	89	78	11	4.01E-01	0.40	0.12
ACGCAA	55	44	11	2.77E-01	0.56	0.11
GTCGTC	65	54	11	3.22E-01	0.49	0.11
CGTCTC	108	97	11	4.51E-01	0.35	0.11
TTGGCT	503	492	11	7.33E-01	0.13	0.11
GCCCAA	266	255	11	6.39E-01	0.19	0.11
ACGTTT	132	121	11	5.02E-01	0.30	0.11
GGTATG	215	204	11	6.02E-01	0.22	0.11
CATCGC	72	61	11	3.55E-01	0.45	0.11
CGAGTA	51	40	11	2.64E-01	0.58	0.11
GCCGTA	48	37	11	2.49E-01	0.60	0.11
GCTATG	270	259	11	6.44E-01	0.19	0.11
GACGCG	31	20	11	1.38E-01	0.86	0.11
GAAGTC	350	339	11	6.87E-01	0.16	0.11
GCGACC	50	39	11	2.64E-01	0.58	0.11
ACAAGA	435	425	10	7.22E-01	0.14	0.11
CTTGGC	454	444	10	7.28E-01	0.14	0.11
AGCGTA	53	43	10	2.87E-01	0.54	0.11
TAGATC	183	173	10	5.82E-01	0.23	0.11
CTGCTA	347	337	10	6.92E-01	0.16	0.11
CTGCAT	474	464	10	7.36E-01	0.13	0.11
CGACCA	56	46	10	3.06E-01	0.51	0.11
CGGCTT	99	89	10	4.52E-01	0.34	0.11
CCAAGA	476	466	10	7.37E-01	0.13	0.11
CCAAGC	379	369	10	7.08E-01	0.15	0.11
TGTCCG	90	80	10	4.33E-01	0.36	0.11
CGGCCCG	96	86	10	4.48E-01	0.35	0.11
TTCTCG	99	89	10	4.60E-01	0.34	0.11
CGAACG	47	37	10	2.69E-01	0.57	0.11
CTCGAC	52	42	10	2.96E-01	0.53	0.11
TCGAGT	69	59	10	3.71E-01	0.43	0.11
TACCGC	44	34	10	2.54E-01	0.60	0.11
CGCCAC	85	75	10	4.26E-01	0.37	0.11
ACGATC	45	35	10	2.64E-01	0.58	0.11
ATCGAA	54	44	10	3.14E-01	0.50	0.11
TCTCGA	73	63	10	3.93E-01	0.41	0.11
ACGCGT	28	18	10	1.44E-01	0.84	0.11
TTGCAG	436	426	10	7.36E-01	0.13	0.11
GATCGA	44	34	10	2.62E-01	0.58	0.11
TTACGG	55	45	10	3.23E-01	0.49	0.10
ACGAAT	59	49	10	3.42E-01	0.47	0.10
CCGCTC	103	93	10	4.81E-01	0.32	0.10
CACGCT	105	95	10	4.86E-01	0.31	0.10
CGGTCC	75	65	10	4.10E-01	0.39	0.10
GCGGTT	63	53	10	3.67E-01	0.44	0.10
CGCCTA	49	39	10	3.00E-01	0.52	0.10
AGATGT	511	501	10	7.61E-01	0.12	0.10
GCGTAC	34	24	10	2.07E-01	0.68	0.10
GAAACT	460	450	10	7.50E-01	0.13	0.10
AACACT	459	449	10	7.50E-01	0.13	0.10
GGCGCT	99	89	10	4.85E-01	0.31	0.10
ATACCG	44	34	10	2.80E-01	0.55	0.10
TAACCG	49	39	10	3.10E-01	0.51	0.10

GTTGAC	211	201	10	6.39E-01	0.19	0.10
CGTACC	44	34	10	2.82E-01	0.55	0.10
CTTGTA	382	372	10	7.29E-01	0.14	0.10
CCCCTT	458	448	10	7.52E-01	0.12	0.10
GGTCGG	68	59	9	3.99E-01	0.40	0.10
CAATCG	42	33	9	2.72E-01	0.57	0.10
CCGTCA	76	67	9	4.28E-01	0.37	0.10
GGCACG	86	77	9	4.59E-01	0.34	0.10
ATGAGC	304	295	9	7.00E-01	0.15	0.10
CCGCAC	77	68	9	4.34E-01	0.36	0.10
CTACGG	54	45	9	3.47E-01	0.46	0.10
CCACGT	132	123	9	5.59E-01	0.25	0.10
TCGAAT	52	43	9	3.39E-01	0.47	0.10
CACGTC	90	81	9	4.77E-01	0.32	0.10
TAACGG	52	43	9	3.45E-01	0.46	0.10
CGTTTC	115	106	9	5.36E-01	0.27	0.10
TACGAG	46	37	9	3.14E-01	0.50	0.10
CTCGCT	113	104	9	5.35E-01	0.27	0.10
GACCAT	272	263	9	6.93E-01	0.16	0.10
CGAGTC	76	67	9	4.46E-01	0.35	0.10
CGTCAT	75	66	9	4.44E-01	0.35	0.10
GGCGTT	71	62	9	4.32E-01	0.36	0.10
CGACGA	21	12	9	1.16E-01	0.94	0.10
TTCGTC	60	51	9	3.93E-01	0.41	0.10
CGTCAC	77	68	9	4.56E-01	0.34	0.10
CGTGCG	41	32	9	2.98E-01	0.53	0.09
AGTCGT	65	56	9	4.19E-01	0.38	0.09
CGACTT	68	59	9	4.33E-01	0.36	0.09
TTCGTG	96	87	9	5.15E-01	0.29	0.09
CTACGC	42	33	9	3.10E-01	0.51	0.09
GCGTAG	47	38	9	3.41E-01	0.47	0.09
CCGGTA	43	34	9	3.18E-01	0.50	0.09
CGCTTT	95	86	9	5.16E-01	0.29	0.09
ATGTTG	404	395	9	7.58E-01	0.12	0.09
GCGTTA	45	36	9	3.38E-01	0.47	0.09
ACGCAT	62	53	9	4.22E-01	0.38	0.09
AGGCCG	83	74	9	4.93E-01	0.31	0.09
CTAGAG	363	354	9	7.48E-01	0.13	0.09
TACCGT	62	53	9	4.27E-01	0.37	0.09
GTACGA	36	27	9	2.84E-01	0.55	0.09
TGCGCG	40	31	9	3.14E-01	0.50	0.09
ACCGTC	68	60	8	4.52E-01	0.34	0.09
TAATCG	43	35	8	3.37E-01	0.47	0.09
AATACG	58	50	8	4.18E-01	0.38	0.09
ACACGT	120	112	8	5.81E-01	0.24	0.09
GCAGTC	298	290	8	7.29E-01	0.14	0.09
GCCGAA	52	44	8	3.94E-01	0.40	0.09
TCGTTG	70	62	8	4.68E-01	0.33	0.09
GACCGC	57	49	8	4.18E-01	0.38	0.09
CTTCGC	68	60	8	4.63E-01	0.33	0.09
TCGCCA	77	69	8	4.94E-01	0.31	0.09
CTTGGT	461	453	8	7.85E-01	0.11	0.09
CGACAC	54	46	8	4.09E-01	0.39	0.09
CCGAGC	104	96	8	5.62E-01	0.25	0.09

GTACGT	57	49	8	4.26E-01	0.37	0.09
CGACGC	23	15	8	1.85E-01	0.73	0.09
ACGCGC	30	22	8	2.60E-01	0.59	0.09
CATACG	54	46	8	4.19E-01	0.38	0.09
CAACGC	52	44	8	4.12E-01	0.38	0.09
CGCTTG	79	71	8	5.14E-01	0.29	0.08
CGATGT	72	64	8	4.93E-01	0.31	0.08
TCAGGC	385	377	8	7.72E-01	0.11	0.08
AACGGT	68	60	8	4.81E-01	0.32	0.08
AACAGG	421	413	8	7.83E-01	0.11	0.08
CTTAGA	390	382	8	7.76E-01	0.11	0.08
TAGCCT	332	324	8	7.58E-01	0.12	0.08
AAAAGG	578	570	8	8.17E-01	0.09	0.08
GGTCGA	39	31	8	3.48E-01	0.46	0.08
CTCGCC	102	94	8	5.75E-01	0.24	0.08
GCACGA	56	48	8	4.46E-01	0.35	0.08
ATTCGC	40	32	8	3.64E-01	0.44	0.08
GACTAA	208	200	8	7.03E-01	0.15	0.08
CGATGA	67	59	8	4.97E-01	0.30	0.08
TCCGTA	58	50	8	4.64E-01	0.33	0.08
TGGCGC	78	70	8	5.34E-01	0.27	0.08
TCGAAG	69	61	8	5.09E-01	0.29	0.08
GTTCGA	40	32	8	3.77E-01	0.42	0.08
GTCCGA	50	42	8	4.35E-01	0.36	0.08
AACGGC	57	50	7	4.69E-01	0.33	0.08
ACGTCC	66	59	7	5.04E-01	0.30	0.08
ACGGCG	27	20	7	2.75E-01	0.56	0.08
GCGCAC	66	59	7	5.06E-01	0.30	0.08
TCGCGT	21	14	7	2.07E-01	0.68	0.08
CGGTAT	44	37	7	4.10E-01	0.39	0.08
CGAACG	81	74	7	5.54E-01	0.26	0.08
CTGCGA	75	68	7	5.43E-01	0.26	0.08
AACACG	94	87	7	5.89E-01	0.23	0.08
TCGACG	17	10	7	1.63E-01	0.79	0.08
GTGTAA	324	317	7	7.75E-01	0.11	0.08
TGCGCC	71	64	7	5.39E-01	0.27	0.08
CTATGC	216	209	7	7.30E-01	0.14	0.08
CGATCG	17	10	7	1.70E-01	0.77	0.08
ATCGTA	47	40	7	4.46E-01	0.35	0.08
CGGGTA	53	46	7	4.75E-01	0.32	0.08
ATACGC	39	32	7	3.99E-01	0.40	0.08
CGCCGG	39	32	7	3.99E-01	0.40	0.08
GCGGTC	53	46	7	4.77E-01	0.32	0.07
AACCGT	72	65	7	5.46E-01	0.26	0.07
CACGCG	38	31	7	3.95E-01	0.40	0.07
CCGTAC	43	36	7	4.27E-01	0.37	0.07
GCGTAT	43	36	7	4.30E-01	0.37	0.07
TACGCT	47	40	7	4.52E-01	0.34	0.07
CGCATA	40	33	7	4.12E-01	0.38	0.07
GATCCC	213	206	7	7.32E-01	0.14	0.07
GTGCAT	333	326	7	7.85E-01	0.10	0.07
CGATCC	49	42	7	4.64E-01	0.33	0.07
GTGCCA	368	361	7	7.96E-01	0.10	0.07
GCCGCG	46	39	7	4.50E-01	0.35	0.07

TAGCCG	52	45	7	4.79E-01	0.32	0.07
ATGACT	379	372	7	7.99E-01	0.10	0.07
CGTCGG	26	19	7	2.99E-01	0.52	0.07
CATTCG	68	61	7	5.45E-01	0.26	0.07
CCCTTC	556	549	7	8.38E-01	0.08	0.07
AGTGAA	485	478	7	8.26E-01	0.08	0.07
TAGGCG	45	38	7	4.57E-01	0.34	0.07
TTATCG	44	37	7	4.51E-01	0.35	0.07
GTGCGC	76	69	7	5.73E-01	0.24	0.07
CGTCGA	17	10	7	1.94E-01	0.71	0.07
ACCCGC	66	59	7	5.45E-01	0.26	0.07
CGATAG	38	31	7	4.17E-01	0.38	0.07
CCTCCT	717	710	7	8.58E-01	0.07	0.07
GCCCCG	93	86	7	6.15E-01	0.21	0.07
CCGACC	67	60	7	5.50E-01	0.26	0.07
GGTACC	189	182	7	7.28E-01	0.14	0.07
CGCTAC	41	34	7	4.40E-01	0.36	0.07
CGCGAC	20	13	7	2.49E-01	0.60	0.07
GCACCC	262	255	7	7.70E-01	0.11	0.07
CGTTAA	56	49	7	5.20E-01	0.28	0.07
ACTAGG	222	215	7	7.52E-01	0.12	0.07
CTACCG	52	45	7	5.04E-01	0.30	0.07
CCTTAC	263	256	7	7.73E-01	0.11	0.07
ACGCGA	19	12	7	2.43E-01	0.61	0.07
GATGTC	313	306	7	7.93E-01	0.10	0.07
GCGACG	22	15	7	2.86E-01	0.54	0.07
GCGCTC	84	77	7	6.08E-01	0.22	0.07
GAACAT	376	369	7	8.12E-01	0.09	0.07
TTCACG	93	87	6	6.29E-01	0.20	0.07
TAACTG	361	355	6	8.09E-01	0.09	0.07
CTGCCA	608	602	6	8.53E-01	0.07	0.07
CGGTAC	43	37	6	4.70E-01	0.33	0.07
CGTTCG	20	14	6	2.68E-01	0.57	0.07
AACGCC	57	51	6	5.37E-01	0.27	0.07
AAGAGT	434	428	6	8.27E-01	0.08	0.07
CGAAAA	58	52	6	5.49E-01	0.26	0.07
TTAGCG	50	44	6	5.17E-01	0.29	0.07
ATGCCG	62	56	6	5.70E-01	0.24	0.07
AAATGG	548	542	6	8.52E-01	0.07	0.07
TTCGCC	51	45	6	5.31E-01	0.28	0.07
AGCGAT	63	57	6	5.75E-01	0.24	0.07
CAAAGA	556	550	6	8.54E-01	0.07	0.06
TCACGT	113	107	6	6.79E-01	0.17	0.06
CGACGT	20	14	6	2.94E-01	0.53	0.06
CTCAGA	654	648	6	8.66E-01	0.06	0.06
TAGGTG	269	263	6	7.91E-01	0.10	0.06
CCTTCC	741	735	6	8.74E-01	0.06	0.06
TAACGT	72	66	6	6.05E-01	0.22	0.06
CCGCAT	56	50	6	5.56E-01	0.25	0.06
CGAGCG	36	30	6	4.56E-01	0.34	0.06
GGCTTC	469	463	6	8.43E-01	0.07	0.06
CGATAC	32	26	6	4.28E-01	0.37	0.06
TCAACG	51	45	6	5.38E-01	0.27	0.06
GCGCTA	41	35	6	4.90E-01	0.31	0.06

CGCTAT	39	33	6	4.82E-01	0.32	0.06
CCTGGT	482	476	6	8.48E-01	0.07	0.06
CGCGGC	43	37	6	5.08E-01	0.29	0.06
ACGTCG	20	14	6	3.12E-01	0.51	0.06
CGAAAG	69	63	6	6.08E-01	0.22	0.06
CCCGAG	144	138	6	7.28E-01	0.14	0.06
CACGAG	96	90	6	6.73E-01	0.17	0.06
TCATCG	70	64	6	6.19E-01	0.21	0.06
CGCCCC	44	38	6	5.26E-01	0.28	0.06
GGGTAA	213	207	6	7.81E-01	0.11	0.06
CCACCT	511	505	6	8.59E-01	0.07	0.06
GCCTTT	567	561	6	8.66E-01	0.06	0.06
ACGACG	21	15	6	3.47E-01	0.46	0.06
TACTGC	271	265	6	8.08E-01	0.09	0.06
TCGTGC	69	63	6	6.25E-01	0.20	0.06
AATCGC	43	37	6	5.31E-01	0.27	0.06
TCGCAA	38	32	6	5.08E-01	0.29	0.06
AGTCG	49	43	6	5.64E-01	0.25	0.06
ACACGC	85	79	6	6.66E-01	0.18	0.06
TGAGGT	432	427	5	8.51E-01	0.07	0.06
GAATCT	335	330	5	8.31E-01	0.08	0.06
AAACGT	116	111	5	7.15E-01	0.15	0.06
ATAGCG	41	36	5	5.37E-01	0.27	0.06
CCTTGA	410	405	5	8.51E-01	0.07	0.06
ATCCGA	50	45	5	5.85E-01	0.23	0.06
CACGAT	62	57	5	6.26E-01	0.20	0.06
AGCCCA	508	503	5	8.68E-01	0.06	0.06
ATCGAG	58	53	5	6.18E-01	0.21	0.06
CGACAT	49	44	5	5.87E-01	0.23	0.06
AAGTGA	478	473	5	8.65E-01	0.06	0.06
CGTAAG	52	47	5	6.00E-01	0.22	0.06
ATGTGC	371	366	5	8.48E-01	0.07	0.06
CGCTTA	44	39	5	5.70E-01	0.24	0.05
CGCCCA	95	90	5	7.05E-01	0.15	0.05
GACACA	440	435	5	8.62E-01	0.06	0.05
GCGCAA	36	31	5	5.33E-01	0.27	0.05
TCGGTA	48	43	5	5.93E-01	0.23	0.05
CGCGTT	20	15	5	3.90E-01	0.41	0.05
GGTGCG	65	60	5	6.52E-01	0.19	0.05
CGCCGC	51	46	5	6.11E-01	0.21	0.05
CCGCGG	46	41	5	5.94E-01	0.23	0.05
CCGTCC	97	92	5	7.19E-01	0.14	0.05
CCGTTT	110	105	5	7.38E-01	0.13	0.05
CGATTG	45	40	5	5.98E-01	0.22	0.05
ATCCGT	64	59	5	6.61E-01	0.18	0.05
CCGATC	39	34	5	5.72E-01	0.24	0.05
TACGAT	42	37	5	5.88E-01	0.23	0.05
TCGCTA	41	36	5	5.86E-01	0.23	0.05
CGCGAT	15	10	5	3.41E-01	0.47	0.05
ACAGCA	580	575	5	8.89E-01	0.05	0.05
CGGTG	19	14	5	4.12E-01	0.39	0.05
TCTTCG	83	78	5	7.09E-01	0.15	0.05
TAGACC	189	184	5	8.07E-01	0.09	0.05
GCGTCG	22	17	5	4.52E-01	0.34	0.05

TCCCGC	91	86	5	7.24E-01	0.14	0.05
TTCGCA	50	45	5	6.31E-01	0.20	0.05
GTATCG	35	30	5	5.63E-01	0.25	0.05
GCTCTC	439	434	5	8.74E-01	0.06	0.05
TCGCCC	70	65	5	6.91E-01	0.16	0.05
GCAAGT	273	268	5	8.44E-01	0.07	0.05
TAAGCG	45	40	5	6.24E-01	0.20	0.05
ACCCGA	70	65	5	6.97E-01	0.16	0.05
TTGCGC	41	36	5	6.09E-01	0.22	0.05
CCGTAT	47	42	5	6.34E-01	0.20	0.05
TCGACA	47	43	4	6.37E-01	0.20	0.05
CATGGC	396	392	4	8.75E-01	0.06	0.05
ATCGCT	64	60	4	6.93E-01	0.16	0.05
AGCGCG	33	29	4	5.79E-01	0.24	0.05
CTGAGT	532	528	4	8.94E-01	0.05	0.05
TCGACC	37	33	4	6.02E-01	0.22	0.05
CTGTTT	815	811	4	9.15E-01	0.04	0.05
TACGGT	48	44	4	6.53E-01	0.19	0.05
TCGCAT	45	41	4	6.43E-01	0.19	0.05
GGCATA	184	180	4	8.23E-01	0.08	0.05
ACAAGC	311	307	4	8.64E-01	0.06	0.05
AGACAA	466	462	4	8.91E-01	0.05	0.04
GGCGAA	44	40	4	6.51E-01	0.19	0.04
CGATCT	48	44	4	6.72E-01	0.17	0.04
CCGCGA	22	18	4	5.20E-01	0.28	0.04
CGAAGT	58	54	4	7.04E-01	0.15	0.04
CGGCGA	23	19	4	5.37E-01	0.27	0.04
GGGTAT	194	190	4	8.42E-01	0.07	0.04
TCAGCG	96	92	4	7.76E-01	0.11	0.04
CTGGTT	462	458	4	8.99E-01	0.05	0.04
CTGTTC	534	530	4	9.08E-01	0.04	0.04
AGTCGC	51	47	4	7.06E-01	0.15	0.04
CCGATA	31	27	4	6.25E-01	0.20	0.04
CCAAG	524	520	4	9.08E-01	0.04	0.04
GTCGCG	17	13	4	4.98E-01	0.30	0.04
TTGGCG	63	59	4	7.40E-01	0.13	0.04
CCCGCG	42	38	4	6.86E-01	0.16	0.04
TACCGG	37	33	4	6.72E-01	0.17	0.04
GCGTAA	31	27	4	6.45E-01	0.19	0.04
ACGTCT	88	84	4	7.89E-01	0.10	0.04
TCGATC	36	32	4	6.71E-01	0.17	0.04
GATCGC	35	31	4	6.66E-01	0.18	0.04
TACGAA	46	43	3	7.12E-01	0.15	0.04
AAAGAC	468	465	3	9.11E-01	0.04	0.04
CCGCGT	28	25	3	6.38E-01	0.19	0.04
CGTACG	14	11	3	4.93E-01	0.31	0.04
TTCGCG	14	11	3	4.97E-01	0.30	0.04
TACTTG	341	338	3	8.97E-01	0.05	0.04
TCGACT	43	40	3	7.12E-01	0.15	0.04
CCGAAT	54	51	3	7.44E-01	0.13	0.04
CGAATT	46	43	3	7.23E-01	0.14	0.04
GGTACG	36	33	3	6.89E-01	0.16	0.04
TATCGG	31	28	3	6.68E-01	0.18	0.03
AGAGTA	327	324	3	8.98E-01	0.05	0.03

TCCGAT	49	46	3	7.41E-01	0.13	0.03
CACGTA	71	68	3	7.86E-01	0.10	0.03
CGCGTA	12	9	3	4.95E-01	0.31	0.03
CGAAC	44	41	3	7.38E-01	0.13	0.03
AGTGC	65	62	3	7.89E-01	0.10	0.03
TTACGC	32	29	3	6.99E-01	0.16	0.03
ACTTGT	429	426	3	9.18E-01	0.04	0.03
CGCATC	53	50	3	7.68E-01	0.11	0.03
AATTCTG	44	41	3	7.47E-01	0.13	0.03
CGCGAA	14	11	3	5.60E-01	0.25	0.03
ACTCAG	486	483	3	9.26E-01	0.03	0.03
CGTAAA	51	48	3	7.72E-01	0.11	0.03
CCGCTA	38	35	3	7.39E-01	0.13	0.03
CGGCAC	63	60	3	7.98E-01	0.10	0.03
CAAGAA	531	528	3	9.31E-01	0.03	0.03
TTCCGA	72	69	3	8.15E-01	0.09	0.03
GTTCCG	59	56	3	7.98E-01	0.10	0.03
CGCGCA	30	27	3	7.21E-01	0.14	0.03
CGCCGT	26	23	3	7.07E-01	0.15	0.03
ACCCCCA	471	468	3	9.32E-01	0.03	0.03
GTTGCC	250	247	3	9.08E-01	0.04	0.03
CACGAA	70	67	3	8.27E-01	0.08	0.03
GACTCA	323	320	3	9.20E-01	0.04	0.03
GTAGCG	42	39	3	7.80E-01	0.11	0.03
GGCACCC	263	260	3	9.13E-01	0.04	0.03
ACGCC	70	68	2	8.33E-01	0.08	0.03
CGGATA	33	31	2	7.60E-01	0.12	0.03
CGTTAC	43	41	2	7.91E-01	0.10	0.03
CAACGG	52	50	2	8.11E-01	0.09	0.03
CATCGT	82	80	2	8.51E-01	0.07	0.03
CGGCGT	24	22	2	7.27E-01	0.14	0.02
TCGCGA	11	9	2	5.95E-01	0.23	0.02
ATTCCG	55	53	2	8.26E-01	0.08	0.02
ACCATG	388	386	2	9.35E-01	0.03	0.02
CCATCG	77	75	2	8.54E-01	0.07	0.02
TCCGCA	63	61	2	8.39E-01	0.08	0.02
AGCAGT	500	498	2	9.44E-01	0.03	0.02
CAACCG	50	48	2	8.25E-01	0.08	0.02
GGTAGT	191	189	2	9.11E-01	0.04	0.02
ACGAGT	56	54	2	8.35E-01	0.08	0.02
GGTACT	200	198	2	9.15E-01	0.04	0.02
TTGGCA	392	390	2	9.40E-01	0.03	0.02
TAGCGA	40	38	2	8.15E-01	0.09	0.02
GCGCCG	36	34	2	8.07E-01	0.09	0.02
CGGGTC	71	69	2	8.64E-01	0.06	0.02
CTGGTA	300	298	2	9.35E-01	0.03	0.02
GCGAAA	36	34	2	8.17E-01	0.09	0.02
TATCGA	34	32	2	8.16E-01	0.09	0.02
GCCTAC	182	180	2	9.22E-01	0.04	0.02
CTAGCG	40	38	2	8.33E-01	0.08	0.02
CCTCCG	129	127	2	9.08E-01	0.04	0.02
CCCGTC	82	80	2	8.85E-01	0.05	0.02
CGCACG	30	28	2	8.13E-01	0.09	0.02
TCCCCG	100	98	2	8.98E-01	0.05	0.02

GTAACC	168	166	2	9.22E-01	0.04	0.02
ACGTTA	63	61	2	8.73E-01	0.06	0.02
TGCAAC	199	197	2	9.30E-01	0.03	0.02
GTAATC	145	143	2	9.19E-01	0.04	0.02
TGCGTA	46	44	2	8.56E-01	0.07	0.02
AGTACG	38	36	2	8.46E-01	0.07	0.02
CGGCTA	40	38	2	8.52E-01	0.07	0.02
CTCGAT	52	50	2	8.70E-01	0.06	0.02
CGCTCG	30	28	2	8.31E-01	0.08	0.02
TACCTG	370	368	2	9.52E-01	0.02	0.02
GTACCG	40	38	2	8.55E-01	0.07	0.02
CGTAAC	35	33	2	8.47E-01	0.07	0.02
GAGTCT	393	391	2	9.57E-01	0.02	0.02
AGCAAT	335	333	2	9.53E-01	0.02	0.02
GCCCAC	345	343	2	9.54E-01	0.02	0.02
CCCCCT	390	389	1	9.58E-01	0.02	0.02
TCGTAA	43	42	1	8.73E-01	0.06	0.02
ATGCGT	60	59	1	8.94E-01	0.05	0.02
CTACTG	337	336	1	9.56E-01	0.02	0.02
CCGCCG	45	44	1	8.81E-01	0.05	0.01
GACTTT	468	467	1	9.63E-01	0.02	0.01
GGCCTA	192	191	1	9.43E-01	0.03	0.01
CCCGAC	67	66	1	9.04E-01	0.04	0.01
GCCAAA	342	341	1	9.58E-01	0.02	0.01
CCCGAA	69	68	1	9.09E-01	0.04	0.01
CGCTCC	98	97	1	9.27E-01	0.03	0.01
CGTCGT	21	20	1	8.41E-01	0.08	0.01
ACGGTA	48	47	1	8.98E-01	0.05	0.01
GACAAT	246	245	1	9.56E-01	0.02	0.01
TCGGCG	20	19	1	8.47E-01	0.07	0.01
CGCGCG	37	36	1	8.89E-01	0.05	0.01
CCCGTA	41	40	1	8.96E-01	0.05	0.01
TACGTG	76	75	1	9.25E-01	0.03	0.01
ACATCG	62	61	1	9.17E-01	0.04	0.01
CCCGCC	153	152	1	9.49E-01	0.02	0.01
GGTACA	231	230	1	9.59E-01	0.02	0.01
GCGATT	40	39	1	9.04E-01	0.04	0.01
CCGTCG	19	18	1	8.61E-01	0.06	0.01
CAACGT	60	59	1	9.24E-01	0.03	0.01
ACCGAT	39	38	1	9.06E-01	0.04	0.01
GCTAGC	198	197	1	9.59E-01	0.02	0.01
TAGCGT	49	48	1	9.18E-01	0.04	0.01
TCTGCA	586	585	1	9.77E-01	0.01	0.01
TGGCTT	667	666	1	9.78E-01	0.01	0.01
CACCTC	440	439	1	9.74E-01	0.01	0.01
TGTGTC	591	590	1	9.78E-01	0.01	0.01
GCACTA	172	171	1	9.60E-01	0.02	0.01
CCCACG	127	126	1	9.54E-01	0.02	0.01
TCTCCG	101	100	1	9.48E-01	0.02	0.01
CGCATT	44	43	1	9.24E-01	0.03	0.01
CCAACG	56	55	1	9.33E-01	0.03	0.01
CTGTCT	773	772	1	9.84E-01	0.01	0.01
GATATG	212	211	1	9.69E-01	0.01	0.01
GTCCAG	395	394	1	9.79E-01	0.01	0.01

CATCGA	59	58	1	9.46E-01	0.02	0.01
GCGCGA	17	16	1	9.02E-01	0.04	0.01
TCCTGC	579	578	1	9.84E-01	0.01	0.01
TCCGTC	75	74	1	9.56E-01	0.02	0.01
CGTCCG	23	22	1	9.21E-01	0.04	0.01
CGTTCA	75	74	1	9.60E-01	0.02	0.01
CCGCGC	38	37	1	9.47E-01	0.02	0.01
TCGATA	32	31	1	9.45E-01	0.02	0.01
TCGGCC	67	66	1	9.63E-01	0.02	0.01
AATCGA	44	43	1	9.57E-01	0.02	0.01

Table S2. Putative miR-128 RISC-associated target genes in adult Camk2a-neurons.

Gene name	# Reads in cluster	Genomic position	Strand	Targeting miR	Seed type
<i>Ogfr1</i>	17	1:23368497-23368505	-	mmu-miR-128-3p	8mer
<i>Pgap1</i>	15	1:54474488-54474496	-	mmu-miR-128-3p	8mer
<i>Fam126b</i>	81	1:58529358-58529366	-	mmu-miR-128-3p	8mer
<i>Plekhm3</i>	12	1:64793596-64793604	-	mmu-miR-128-3p	8mer
<i>Plekhm3</i>	12	1:64793635-64793643	-	mmu-miR-128-3p	8mer
<i>Unc80</i>	32	1:66698909-66698917	+	mmu-miR-128-3p	8mer
<i>Irs1</i>	10	1:82237388-82237396	-	mmu-miR-128-3p	8mer
<i>Nfasc</i>	23	1:132567868-132567876	-	mmu-miR-128-3p	8mer
<i>7530420F21Rik</i>	31	1:150076780-150076788	-	mmu-miR-128-3p	8mer
<i>Swt1</i>	11	1:151368199-151368207	-	mmu-miR-128-3p	8mer
<i>Lamc1</i>	11	1:153220197-153220205	-	mmu-miR-128-3p	8mer
<i>Rgs8</i>	81	1:153694067-153694075	+	mmu-miR-128-3p	8mer
<i>Il1dr2</i>	13	1:166315229-166315237	+	mmu-miR-128-3p	8mer
<i>Kcnk2</i>	15	1:189208581-189208589	-	mmu-miR-128-3p	8mer
<i>Tug1</i>	12	11:3645366-3645374	-	mmu-miR-128-3p	8mer
<i>Pex13</i>	28	11:23648703-23648711	-	mmu-miR-128-3p	8mer
<i>Erlec1</i>	227	11:30929829-30929837	-	mmu-miR-128-3p	8mer
<i>Sec24a</i>	14	11:51695032-51695040	-	mmu-miR-128-3p	8mer
<i>Ulk2</i>	14	11:61775839-61775847	-	mmu-miR-128-3p	8mer
<i>Adora2b</i>	14	11:62265795-62265803	+	mmu-miR-128-3p	8mer
<i>Dvl2</i>	28	11:70009708-70009716	+	mmu-miR-128-3p	8mer
<i>1700071K01Rik</i>	10	11:81572558-81572566	-	mmu-miR-128-3p	8mer
<i>Fbxl20</i>	16	11:98085926-98085934	-	mmu-miR-128-3p	8mer
<i>Msl1</i>	17	11:98807582-98807590	+	mmu-miR-128-3p	8mer
<i>Casc3</i>	366	11:98833664-98833672	+	mmu-miR-128-3p	8mer
<i>Ccdc47</i>	41	11:106200261-106200269	-	mmu-miR-128-3p	8mer
<i>H3f3b</i>	14	11:116023028-116023036	-	mmu-miR-128-3p	8mer
<i>Kidins220</i>	14	12:25060225-25060233	+	mmu-miR-128-3p	8mer
<i>Rgs6</i>	22	12:83158068-83158076	+	mmu-miR-128-3p	8mer
<i>Dicer1</i>	10	12:104690348-104690356	-	mmu-miR-128-3p	8mer
<i>Clmn</i>	10	12:104766958-104766966	-	mmu-miR-128-3p	8mer
<i>Dlk1</i>	22	12:109460801-109460809	+	mmu-miR-128-3p	8mer
<i>Tmem179</i>	27	12:112500948-112500956	-	mmu-miR-128-3p	8mer
<i>Slc22a23</i>	39	13:34179265-34179273	-	mmu-miR-128-3p	8mer
<i>Mtx3</i>	22	13:92855392-92855400	+	mmu-miR-128-3p	8mer
<i>Pde8b</i>	39	13:95026091-95026099	-	mmu-miR-128-3p	8mer
<i>Plk2</i>	19	13:110400282-110400290	+	mmu-miR-128-3p	8mer
<i>Snx18</i>	13	13:113593615-113593623	-	mmu-miR-128-3p	8mer
<i>Ercc6</i>	17	14:32577321-32577329	+	mmu-miR-128-3p	8mer
<i>Nupl1</i>	11	14:60218777-60218785	-	mmu-miR-128-3p	8mer
<i>Cct5</i>	40	15:31590905-31590913	-	mmu-miR-128-3p	8mer
<i>Csdc2</i>	11	15:81950592-81950600	+	mmu-miR-128-3p	8mer
<i>1700001L05Rik</i>	33	15:83358847-83358855	-	mmu-miR-128-3p	8mer
<i>Nup50</i>	21	15:84940284-84940292	+	mmu-miR-128-3p	8mer
<i>Nell2</i>	17	15:95218498-95218506	-	mmu-miR-128-3p	8mer
<i>Tvp23a</i>	51	16:10421373-10421381	-	mmu-miR-128-3p	8mer
<i>Ccdc50</i>	29	16:27449454-27449462	+	mmu-miR-128-3p	8mer
<i>Tnk2</i>	147	16:32683208-32683216	+	mmu-miR-128-3p	8mer
<i>Lrch3</i>	21	16:33013539-33013547	+	mmu-miR-128-3p	8mer
<i>Itsn1</i>	149	16:91918670-91918678	+	mmu-miR-128-3p	8mer
<i>Prr18</i>	18	17:8342974-8342982	+	mmu-miR-128-3p	8mer
<i>Pde10a</i>	73	17:8985876-8985884	+	mmu-miR-128-3p	8mer
<i>Pdpk1</i>	68	17:24076069-24076077	-	mmu-miR-128-3p	8mer
<i>Mapk14</i>	21	17:28746530-28746538	+	mmu-miR-128-3p	8mer
<i>Prr3</i>	26	17:35978656-35978664	-	mmu-miR-128-3p	8mer
<i>Plcl2</i>	18	17:50689553-50689561	+	mmu-miR-128-3p	8mer
<i>Myl12b</i>	21	17:70974045-70974053	-	mmu-miR-128-3p	8mer
<i>Arhgap12</i>	13	18:6025918-6025926	-	mmu-miR-128-3p	8mer
<i>Dtna</i>	29	18:23653797-23653805	+	mmu-miR-128-3p	8mer
<i>Elp2</i>	134	18:24638563-24638571	+	mmu-miR-128-3p	8mer
<i>Fads1</i>	248	19:10196570-10196578	+	mmu-miR-128-3p	8mer
<i>Wbp11</i>	26	19:46657343-46657351	+	mmu-miR-128-3p	8mer
<i>Atrnl1</i>	13	19:58133164-58133172	+	mmu-miR-128-3p	8mer

<i>Bmi1</i>	23	2:18684936-18684944	+	mmu-miR-128-3p	8mer
<i>Fam102a</i>	17	2:32567617-32567625	+	mmu-miR-128-3p	8mer
<i>Slc39a13</i>	92	2:91062739-91062747	-	mmu-miR-128-3p	8mer
<i>Madd</i>	34	2:91137970-91137978	-	mmu-miR-128-3p	8mer
<i>Trim44</i>	29	2:102303581-102303589	-	mmu-miR-128-3p	8mer
<i>Dut</i>	16	2:125257564-125257572	+	mmu-miR-128-3p	8mer
<i>Dzank1</i>	32	2:144470922-144470930	-	mmu-miR-128-3p	8mer
<i>Plagl2</i>	15	2:153229052-153229060	-	mmu-miR-128-3p	8mer
<i>Pard6b</i>	17	2:168100923-168100931	+	mmu-miR-128-3p	8mer
<i>Ppp1r3d</i>	17	2:178413235-178413243	-	mmu-miR-128-3p	8mer
<i>Samd10</i>	54	2:181596543-181596551	-	mmu-miR-128-3p	8mer
<i>Oprl1</i>	11	2:181720096-181720104	+	mmu-miR-128-3p	8mer
<i>Zfp704</i>	111	3:9432272-9432280	-	mmu-miR-128-3p	8mer
<i>Vangl1</i>	10	3:102157258-102157266	-	mmu-miR-128-3p	8mer
<i>Slc6a17</i>	20	3:107467878-107467886	-	mmu-miR-128-3p	8mer
<i>Csf1</i>	23	3:107742361-107742369	-	mmu-miR-128-3p	8mer
<i>4933431E20Rik</i>	25	3:107895527-107895535	-	mmu-miR-128-3p	8mer
<i>N28178</i>	12	4:42942134-42942142	+	mmu-miR-128-3p	8mer
<i>E130308A19Rik</i>	20	4:59753649-59753657	+	mmu-miR-128-3p	8mer
<i>6330416G13Rik</i>	39	4:63585622-63585630	+	mmu-miR-128-3p	8mer
<i>Ak4</i>	37	4:101466740-101466748	+	mmu-miR-128-3p	8mer
<i>Ppap2b</i>	48	4:105231683-105231691	+	mmu-miR-128-3p	8mer
<i>Med8</i>	15	4:118414920-118414928	+	mmu-miR-128-3p	8mer
<i>Stk40</i>	24	4:126140285-126140293	+	mmu-miR-128-3p	8mer
<i>5730409E04Rik</i>	23	4:126613703-126613711	+	mmu-miR-128-3p	8mer
<i>Szrd1</i>	16	4:141115562-141115570	-	mmu-miR-128-3p	8mer
<i>Szrd1</i>	16	4:141115590-141115598	-	mmu-miR-128-3p	8mer
<i>Szrd1</i>	16	4:141115612-141115620	-	mmu-miR-128-3p	8mer
<i>Szrd1</i>	16	4:141115636-141115644	-	mmu-miR-128-3p	8mer
<i>Tmem51</i>	18	4:142031578-142031586	-	mmu-miR-128-3p	8mer
<i>Mthfr</i>	86	4:148055973-148055981	+	mmu-miR-128-3p	8mer
<i>Fbxo2</i>	18	4:148167191-148167199	+	mmu-miR-128-3p	8mer
<i>5930403L14Rik</i>	27	4:154633291-154633299	-	mmu-miR-128-3p	8mer
<i>Adam22</i>	17	5:8077056-8077064	-	mmu-miR-128-3p	8mer
<i>Xrcc2</i>	75	5:25691175-25691183	-	mmu-miR-128-3p	8mer
<i>Lmbr1</i>	13	5:29233062-29233070	-	mmu-miR-128-3p	8mer
<i>Sorcs2</i>	25	5:36018257-36018265	-	mmu-miR-128-3p	8mer
<i>Stim2</i>	24	5:54119455-54119463	+	mmu-miR-128-3p	8mer
<i>Limch1</i>	28	5:67054253-67054261	+	mmu-miR-128-3p	8mer
<i>Bend4</i>	31	5:67392837-67392845	-	mmu-miR-128-3p	8mer
<i>Guf1</i>	25	5:69573848-69573856	+	mmu-miR-128-3p	8mer
<i>Rchy1</i>	18	5:91957552-91957560	-	mmu-miR-128-3p	8mer
<i>Sparcl1</i>	27	5:104078687-104078695	-	mmu-miR-128-3p	8mer
<i>Fbrsl1</i>	13	5:110362665-110362673	-	mmu-miR-128-3p	8mer
<i>Med13l</i>	86	5:118762944-118762952	+	mmu-miR-128-3p	8mer
<i>Abcb9</i>	18	5:124062131-124062139	-	mmu-miR-128-3p	8mer
<i>Pitpnm2</i>	23	5:124120220-124120228	-	mmu-miR-128-3p	8mer
<i>Sbno1</i>	28	5:124371329-124371337	-	mmu-miR-128-3p	8mer
<i>Ccdc92</i>	32	5:124835479-124835487	-	mmu-miR-128-3p	8mer
<i>Tmsb10</i>	11	6:72957500-72957508	-	mmu-miR-128-3p	8mer
<i>Slc6a6</i>	47	6:91757507-91757515	+	mmu-miR-128-3p	8mer
<i>Arl8b</i>	97	6:108823215-108823223	+	mmu-miR-128-3p	8mer
<i>Wnk1</i>	43	6:119925717-119925725	-	mmu-miR-128-3p	8mer
<i>Kcna1</i>	13	6:126640031-126640039	-	mmu-miR-128-3p	8mer
<i>Cic</i>	16	7:25294348-25294356	+	mmu-miR-128-3p	8mer
<i>Iglon5</i>	48	7:43474292-43474300	-	mmu-miR-128-3p	8mer
<i>Siglech</i>	12	7:55778178-55778186	+	mmu-miR-128-3p	8mer
<i>Apba2</i>	128	7:64754441-64754449	+	mmu-miR-128-3p	8mer
<i>Trim66</i>	15	7:109453347-109453355	-	mmu-miR-128-3p	8mer
<i>Ndufab1</i>	27	7:122090943-122090951	-	mmu-miR-128-3p	8mer
<i>Prkcb</i>	35	7:122632405-122632413	+	mmu-miR-128-3p	8mer
<i>Ypel3</i>	62	7:126780258-126780266	+	mmu-miR-128-3p	8mer
<i>Map2k7</i>	169	8:4246082-4246090	+	mmu-miR-128-3p	8mer
<i>Mcph1</i>	57	8:18802349-18802357	+	mmu-miR-128-3p	8mer
<i>Car7</i>	39	8:104550010-104550018	+	mmu-miR-128-3p	8mer
<i>Terf2</i>	38	8:107075600-107075608	-	mmu-miR-128-3p	8mer

<i>Elavl3</i>	14	9:22017416-22017424	-	mmu-miR-128-3p	8mer
<i>Arhgap32</i>	63	9:32263491-32263499	+	mmu-miR-128-3p	8mer
<i>Rab27a</i>	20	9:73096052-73096060	+	mmu-miR-128-3p	8mer
<i>Nktr</i>	11	9:121755037-121755045	+	mmu-miR-128-3p	8mer
<i>Pdha1</i>	14	X:160122990-160122998	-	mmu-miR-128-3p	8mer
<i>3110035E14Rik</i>	63	1:9625616-9625623	+	mmu-miR-128-3p	7mer-m8
<i>Smap1</i>	12	1:23845935-23845942	-	mmu-miR-128-3p	7mer-m8
<i>Actr1b</i>	37	1:36698521-36698528	-	mmu-miR-128-3p	7mer-m8
<i>Actr1b</i>	68	1:36699776-36699783	-	mmu-miR-128-3p	7mer-m8
<i>Nrp2</i>	77	1:62796562-62796569	+	mmu-miR-128-3p	7mer-m8
<i>Ino80d</i>	23	1:63053467-63053474	-	mmu-miR-128-3p	7mer-m8
<i>Unc80</i>	67	1:66695833-66695840	+	mmu-miR-128-3p	7mer-m8
<i>Agfg1</i>	46	1:82895183-82895190	+	mmu-miR-128-3p	7mer-m8
<i>Gpc1</i>	40	1:92859147-92859154	+	mmu-miR-128-3p	7mer-m8
<i>Gpc1</i>	40	1:92859187-92859194	+	mmu-miR-128-3p	7mer-m8
<i>Smg7</i>	22	1:152837172-152837179	-	mmu-miR-128-3p	7mer-m8
<i>Smg7</i>	18	1:152838081-152838088	-	mmu-miR-128-3p	7mer-m8
<i>Qsox1</i>	27	1:155778253-155778260	-	mmu-miR-128-3p	7mer-m8
<i>Tor1aip2</i>	19	1:156065553-156065560	+	mmu-miR-128-3p	7mer-m8
<i>Atp1b1</i>	133	1:164437502-164437509	-	mmu-miR-128-3p	7mer-m8
<i>Uck2</i>	15	1:167225255-167225262	-	mmu-miR-128-3p	7mer-m8
<i>Pcp4l1</i>	10	1:171173355-171173362	-	mmu-miR-128-3p	7mer-m8
<i>Ndufs2</i>	11	1:171233983-171233990	-	mmu-miR-128-3p	7mer-m8
<i>Cnih4</i>	20	1:181167474-181167481	+	mmu-miR-128-3p	7mer-m8
<i>Kctd3</i>	26	1:188971628-188971635	-	mmu-miR-128-3p	7mer-m8
<i>Angel2</i>	15	1:190945918-190945925	+	mmu-miR-128-3p	7mer-m8
<i>Tmem206</i>	41	1:191350245-191350252	+	mmu-miR-128-3p	7mer-m8
<i>Lpgat1</i>	85	1:191779082-191779089	+	mmu-miR-128-3p	7mer-m8
<i>Lpgat1</i>	14	1:191782336-191782343	+	mmu-miR-128-3p	7mer-m8
<i>Sf3a1</i>	12	11:4182007-4182014	+	mmu-miR-128-3p	7mer-m8
<i>Nf2</i>	24	11:4767898-4767905	-	mmu-miR-128-3p	7mer-m8
<i>Adcy1</i>	16	11:7171520-7171527	+	mmu-miR-128-3p	7mer-m8
<i>Adcy1</i>	74	11:7173857-7173864	+	mmu-miR-128-3p	7mer-m8
<i>Mgat4b</i>	42	11:50234853-50234860	+	mmu-miR-128-3p	7mer-m8
<i>Ppp2ca</i>	11	11:52122729-52122736	+	mmu-miR-128-3p	7mer-m8
<i>9530068E07Rik</i>	16	11:52408614-52408621	+	mmu-miR-128-3p	7mer-m8
<i>Fxr2</i>	45	11:69653093-69653100	+	mmu-miR-128-3p	7mer-m8
<i>Mnt</i>	17	11:74844108-74844115	+	mmu-miR-128-3p	7mer-m8
<i>Pitpna</i>	26	11:75626363-75626370	+	mmu-miR-128-3p	7mer-m8
<i>Glod4</i>	28	11:76221044-76221051	-	mmu-miR-128-3p	7mer-m8
<i>Sez6</i>	41	11:77978825-77978832	+	mmu-miR-128-3p	7mer-m8
<i>Ppm1e</i>	31	11:87227707-87227714	-	mmu-miR-128-3p	7mer-m8
<i>Zfp652</i>	39	11:95764432-95764439	+	mmu-miR-128-3p	7mer-m8
<i>Sp2</i>	13	11:96953834-96953841	-	mmu-miR-128-3p	7mer-m8
<i>Cwc25</i>	20	11:97747131-97747138	-	mmu-miR-128-3p	7mer-m8
<i>Pgap3</i>	41	11:98389372-98389379	-	mmu-miR-128-3p	7mer-m8
<i>Casc3</i>	366	11:98833688-98833695	+	mmu-miR-128-3p	7mer-m8
<i>Fam134c</i>	21	11:101098135-101098142	-	mmu-miR-128-3p	7mer-m8
<i>Rundc3a</i>	36	11:102401605-102401612	+	mmu-miR-128-3p	7mer-m8
<i>Rundc3a</i>	36	11:102401717-102401724	+	mmu-miR-128-3p	7mer-m8
<i>Arf2</i>	109	11:103984592-103984599	+	mmu-miR-128-3p	7mer-m8
<i>Tanc2</i>	436	11:105927963-105927970	+	mmu-miR-128-3p	7mer-m8
<i>Dcaf7</i>	37	11:106059121-106059128	+	mmu-miR-128-3p	7mer-m8
<i>Ern1</i>	10	11:106397377-106397384	-	mmu-miR-128-3p	7mer-m8
<i>Tex2</i>	54	11:106502851-106502858	-	mmu-miR-128-3p	7mer-m8
<i>Tex2</i>	57	11:106503114-106503121	-	mmu-miR-128-3p	7mer-m8
<i>Polg2</i>	55	11:106781085-106781092	-	mmu-miR-128-3p	7mer-m8
<i>Sox9</i>	33	11:112786519-112786526	+	mmu-miR-128-3p	7mer-m8
<i>H3f3b</i>	14	11:116023221-116023228	-	mmu-miR-128-3p	7mer-m8
<i>Nptx1</i>	11	11:119540017-119540024	-	mmu-miR-128-3p	7mer-m8
<i>Ccdc71l</i>	10	12:32382154-32382161	+	mmu-miR-128-3p	7mer-m8
<i>Nrcam</i>	14	12:44601625-44601632	+	mmu-miR-128-3p	7mer-m8
<i>Sptssa</i>	23	12:54645672-54645679	-	mmu-miR-128-3p	7mer-m8
<i>Sgpp1</i>	17	12:75715472-75715479	-	mmu-miR-128-3p	7mer-m8
<i>Rdh11</i>	17	12:79175255-79175262	-	mmu-miR-128-3p	7mer-m8
<i>Dcaf5</i>	10	12:80337820-80337827	-	mmu-miR-128-3p	7mer-m8

<i>Calm1</i>	101	12:100209638-100209645	+	mmu-miR-128-3p	7mer-m8
<i>Itpk1</i>	35	12:102570160-102570167	-	mmu-miR-128-3p	7mer-m8
<i>D430019H16Rik</i>	21	12:105491959-105491966	+	mmu-miR-128-3p	7mer-m8
<i>Traf3</i>	31	12:111266441-111266448	+	mmu-miR-128-3p	7mer-m8
<i>Traf3</i>	31	12:111266471-111266478	+	mmu-miR-128-3p	7mer-m8
<i>Lyst</i>	72	13:13778047-13778054	+	mmu-miR-128-3p	7mer-m8
<i>Arid4b</i>	10	13:14197990-14197997	+	mmu-miR-128-3p	7mer-m8
<i>Gfod1</i>	16	13:43196102-43196109	-	mmu-miR-128-3p	7mer-m8
<i>Gfod1</i>	15	13:43199793-43199800	-	mmu-miR-128-3p	7mer-m8
<i>Ptpdc1</i>	22	13:48578059-48578066	-	mmu-miR-128-3p	7mer-m8
<i>Phf2</i>	22	13:48802958-48802965	-	mmu-miR-128-3p	7mer-m8
<i>Diras2</i>	34	13:52506151-52506158	-	mmu-miR-128-3p	7mer-m8
<i>Ddx46</i>	22	13:55679395-55679402	+	mmu-miR-128-3p	7mer-m8
<i>Smad5</i>	11	13:56738800-56738807	+	mmu-miR-128-3p	7mer-m8
<i>Ntrk2</i>	10	13:59130314-59130321	+	mmu-miR-128-3p	7mer-m8
<i>Adcy2</i>	159	13:68620520-68620527	-	mmu-miR-128-3p	7mer-m8
<i>Thrb</i>	19	14:18036361-18036368	+	mmu-miR-128-3p	7mer-m8
<i>Samd8</i>	30	14:21798177-21798184	+	mmu-miR-128-3p	7mer-m8
<i>Serp2</i>	22	14:76532915-76532922	-	mmu-miR-128-3p	7mer-m8
<i>Ctnnd2</i>	12	15:31028061-31028068	+	mmu-miR-128-3p	7mer-m8
<i>Ankr33b</i>	18	15:31294385-31294392	-	mmu-miR-128-3p	7mer-m8
<i>Mtdh</i>	14	15:34141902-34141909	+	mmu-miR-128-3p	7mer-m8
<i>Fbxo32</i>	3041	15:58180264-58180271	-	mmu-miR-128-3p	7mer-m8
<i>Rbfox2</i>	27	15:77081501-77081508	-	mmu-miR-128-3p	7mer-m8
<i>Myh9</i>	30	15:77761129-77761136	-	mmu-miR-128-3p	7mer-m8
<i>Syng1</i>	44	15:80119512-80119519	+	mmu-miR-128-3p	7mer-m8
<i>Cacna1i</i>	19	15:80397477-80397484	+	mmu-miR-128-3p	7mer-m8
<i>Xrcc6</i>	43	15:82040046-82040053	+	mmu-miR-128-3p	7mer-m8
<i>Sept3</i>	39	15:82294273-82294280	+	mmu-miR-128-3p	7mer-m8
<i>Nup50</i>	23	15:84942041-84942048	+	mmu-miR-128-3p	7mer-m8
<i>Tubgcp6</i>	15	15:89100178-89100185	-	mmu-miR-128-3p	7mer-m8
<i>Ncaph2</i>	11	15:89371692-89371699	+	mmu-miR-128-3p	7mer-m8
<i>Lmbr1l</i>	82	15:98904027-98904034	-	mmu-miR-128-3p	7mer-m8
<i>Letmd1</i>	11	15:100478931-100478938	+	mmu-miR-128-3p	7mer-m8
<i>Sp1</i>	10	15:102432504-102432511	+	mmu-miR-128-3p	7mer-m8
<i>Sp1</i>	14	15:102435737-102435744	+	mmu-miR-128-3p	7mer-m8
<i>Pde1b</i>	24	15:103528987-103528994	+	mmu-miR-128-3p	7mer-m8
<i>Ppp1r1a</i>	17	15:103530439-103530446	-	mmu-miR-128-3p	7mer-m8
<i>Glyr1</i>	22	16:5014123-5014130	-	mmu-miR-128-3p	7mer-m8
<i>Snn</i>	94	16:11074509-11074516	+	mmu-miR-128-3p	7mer-m8
<i>Mapk1</i>	19	16:17046124-17046131	+	mmu-miR-128-3p	7mer-m8
<i>2510009E07Rik</i>	26	16:21649463-21649470	-	mmu-miR-128-3p	7mer-m8
<i>2510009E07Rik</i>	10	16:21653204-21653211	-	mmu-miR-128-3p	7mer-m8
<i>Ccdc50</i>	358	16:27451794-27451801	+	mmu-miR-128-3p	7mer-m8
<i>Lsg1</i>	45	16:30561574-30561581	-	mmu-miR-128-3p	7mer-m8
<i>Ppp1r2</i>	42	16:31253491-31253498	-	mmu-miR-128-3p	7mer-m8
<i>Lrrc58</i>	50	16:37882992-37882999	+	mmu-miR-128-3p	7mer-m8
<i>Gm608</i>	37	16:44222955-44222962	+	mmu-miR-128-3p	7mer-m8
<i>Cpox</i>	15	16:58678812-58678819	+	mmu-miR-128-3p	7mer-m8
<i>Cpox</i>	15	16:58678821-58678828	+	mmu-miR-128-3p	7mer-m8
<i>Rcan1</i>	44	16:92393344-92393351	-	mmu-miR-128-3p	7mer-m8
<i>Pisd-ps2</i>	25	17:3079599-3079606	-	mmu-miR-128-3p	7mer-m8
<i>Tulp4</i>	10	17:6239696-6239703	+	mmu-miR-128-3p	7mer-m8
<i>Srsf3</i>	10	17:29041794-29041801	+	mmu-miR-128-3p	7mer-m8
<i>Srsf3</i>	10	17:29041802-29041809	+	mmu-miR-128-3p	7mer-m8
<i>Mtch1</i>	31	17:29332177-29332184	-	mmu-miR-128-3p	7mer-m8
<i>Tbc1d22b</i>	58	17:29606379-29606386	+	mmu-miR-128-3p	7mer-m8
<i>Tmem151b</i>	60	17:45542031-45542038	-	mmu-miR-128-3p	7mer-m8
<i>Med20</i>	12	17:47623824-47623831	+	mmu-miR-128-3p	7mer-m8
<i>Fem1a</i>	13	17:56263557-56263564	+	mmu-miR-128-3p	7mer-m8
<i>Soga2</i>	10	17:66336532-66336539	-	mmu-miR-128-3p	7mer-m8
<i>Sos1</i>	19	17:80396697-80396704	-	mmu-miR-128-3p	7mer-m8
<i>Tmem178</i>	24	17:81001481-81001488	+	mmu-miR-128-3p	7mer-m8
<i>Kif5b</i>	52	18:6203450-6203457	-	mmu-miR-128-3p	7mer-m8
<i>Rab18</i>	20	18:6791112-6791119	+	mmu-miR-128-3p	7mer-m8
<i>Syt4</i>	2619	18:31439514-31439521	-	mmu-miR-128-3p	7mer-m8

<i>Paip2</i>	37	18:35616347-35616354	+	mmu-miR-128-3p	7mer-m8
<i>Fgf1</i>	47	18:38841082-38841089	-	mmu-miR-128-3p	7mer-m8
<i>Ndst1</i>	41	18:60687202-60687209	-	mmu-miR-128-3p	7mer-m8
<i>St8sia3</i>	29	18:64275798-64275805	+	mmu-miR-128-3p	7mer-m8
<i>Onecut2</i>	10	18:64388493-64388500	+	mmu-miR-128-3p	7mer-m8
<i>Nedd4l</i>	31	18:65215568-65215575	+	mmu-miR-128-3p	7mer-m8
<i>Tcf4</i>	15	18:69683400-69683407	+	mmu-miR-128-3p	7mer-m8
<i>Tcf4</i>	10	18:69684171-69684178	+	mmu-miR-128-3p	7mer-m8
<i>Atp9b</i>	23	18:80736093-80736100	-	mmu-miR-128-3p	7mer-m8
<i>Zfp516</i>	24	18:83001690-83001697	+	mmu-miR-128-3p	7mer-m8
<i>Zfp516</i>	11	18:83002517-83002524	+	mmu-miR-128-3p	7mer-m8
<i>Cndp2</i>	10	18:84667612-84667619	-	mmu-miR-128-3p	7mer-m8
<i>Naa40</i>	100	19:7227966-7227973	-	mmu-miR-128-3p	7mer-m8
<i>Fads1</i>	248	19:10196544-10196551	+	mmu-miR-128-3p	7mer-m8
<i>Dagla</i>	16	19:10246661-10246668	-	mmu-miR-128-3p	7mer-m8
<i>Syt7</i>	64	19:10451081-10451088	+	mmu-miR-128-3p	7mer-m8
<i>Dtx4</i>	47	19:12469031-12469038	-	mmu-miR-128-3p	7mer-m8
<i>Trpm3</i>	92	19:22990278-22990285	+	mmu-miR-128-3p	7mer-m8
<i>Ak3</i>	10	19:29021780-29021787	-	mmu-miR-128-3p	7mer-m8
<i>March5</i>	38	19:37222449-37222456	+	mmu-miR-128-3p	7mer-m8
<i>Slit1</i>	38	19:41599511-41599518	-	mmu-miR-128-3p	7mer-m8
<i>Golga7b</i>	64	19:42269184-42269191	+	mmu-miR-128-3p	7mer-m8
<i>Arl3</i>	19	19:46530872-46530879	-	mmu-miR-128-3p	7mer-m8
<i>Sh3pxd2a</i>	15	19:47265824-47265831	-	mmu-miR-128-3p	7mer-m8
<i>Cacul1</i>	10	19:60527075-60527082	-	mmu-miR-128-3p	7mer-m8
<i>Prpf18</i>	21	2:4621713-4621720	-	mmu-miR-128-3p	7mer-m8
<i>5031426D15Rik</i>	16	2:6927244-6927251	-	mmu-miR-128-3p	7mer-m8
<i>Nacc2</i>	21	2:26058181-26058188	-	mmu-miR-128-3p	7mer-m8
<i>Sdccag3</i>	31	2:26383155-26383162	-	mmu-miR-128-3p	7mer-m8
<i>Fnbp1</i>	11	2:31028497-31028504	-	mmu-miR-128-3p	7mer-m8
<i>Rab14</i>	39	2:35181312-35181319	-	mmu-miR-128-3p	7mer-m8
<i>Dab2ip</i>	30	2:35730791-35730798	+	mmu-miR-128-3p	7mer-m8
<i>Ttll11</i>	15	2:35751523-35751530	-	mmu-miR-128-3p	7mer-m8
<i>Ttll11</i>	15	2:35751537-35751544	-	mmu-miR-128-3p	7mer-m8
<i>B3galt1</i>	10	2:68119192-68119199	+	mmu-miR-128-3p	7mer-m8
<i>Pdk1</i>	19	2:71902933-71902940	+	mmu-miR-128-3p	7mer-m8
<i>Sestd1</i>	21	2:77180784-77180791	-	mmu-miR-128-3p	7mer-m8
<i>Dnajc10</i>	33	2:80353014-80353021	+	mmu-miR-128-3p	7mer-m8
<i>Madd</i>	34	2:91137862-91137869	-	mmu-miR-128-3p	7mer-m8
<i>Madd</i>	34	2:91137933-91137940	-	mmu-miR-128-3p	7mer-m8
<i>Hipk3</i>	30	2:104426705-104426712	-	mmu-miR-128-3p	7mer-m8
<i>Vps39</i>	14	2:120343177-120343184	-	mmu-miR-128-3p	7mer-m8
<i>B2m</i>	26	2:122153000-122153007	+	mmu-miR-128-3p	7mer-m8
<i>Tmem87b</i>	16	2:128852582-128852589	+	mmu-miR-128-3p	7mer-m8
<i>Prnp</i>	54	2:131938125-131938132	+	mmu-miR-128-3p	7mer-m8
<i>Cds2</i>	72	2:132310931-132310938	+	mmu-miR-128-3p	7mer-m8
<i>Insm1</i>	35	2:146224745-146224752	+	mmu-miR-128-3p	7mer-m8
<i>Napb</i>	15	2:148695067-148695074	-	mmu-miR-128-3p	7mer-m8
<i>Acss1</i>	12	2:150618613-150618620	-	mmu-miR-128-3p	7mer-m8
<i>Pygb</i>	34	2:150831594-150831601	+	mmu-miR-128-3p	7mer-m8
<i>Epb4.1I1</i>	23	2:156540701-156540708	+	mmu-miR-128-3p	7mer-m8
<i>9830001H06Rik</i>	14	2:157011152-157011159	-	mmu-miR-128-3p	7mer-m8
<i>Ralgapb</i>	36	2:158496067-158496074	+	mmu-miR-128-3p	7mer-m8
<i>Ppp1r16b</i>	57	2:158763552-158763559	+	mmu-miR-128-3p	7mer-m8
<i>Chd6</i>	20	2:160948946-160948953	-	mmu-miR-128-3p	7mer-m8
<i>Sdc4</i>	59	2:164424791-164424798	-	mmu-miR-128-3p	7mer-m8
<i>Stx16</i>	13	2:174097094-174097101	+	mmu-miR-128-3p	7mer-m8
<i>Ythdf1</i>	29	2:180904780-180904787	-	mmu-miR-128-3p	7mer-m8
<i>Arfrp1</i>	12	2:181364085-181364092	-	mmu-miR-128-3p	7mer-m8
<i>Slc7a14</i>	24	3:31205498-31205505	-	mmu-miR-128-3p	7mer-m8
<i>Zmat3</i>	12	3:32340182-32340189	-	mmu-miR-128-3p	7mer-m8
<i>Larp1b</i>	25	3:40977943-40977950	+	mmu-miR-128-3p	7mer-m8
<i>Slc7a11</i>	20	3:50368055-50368062	-	mmu-miR-128-3p	7mer-m8
<i>Naa15</i>	11	3:51473314-51473321	+	mmu-miR-128-3p	7mer-m8
<i>Setd7</i>	23	3:51515933-51515940	-	mmu-miR-128-3p	7mer-m8
<i>Setd7</i>	255	3:51518367-51518374	-	mmu-miR-128-3p	7mer-m8

<i>Npy2r</i>	15	3:82539975-82539982	-	mmu-miR-128-3p	7mer-m8
<i>Cct3</i>	14	3:88321617-88321624	+	mmu-miR-128-3p	7mer-m8
<i>Syt11</i>	18	3:88745929-88745936	-	mmu-miR-128-3p	7mer-m8
<i>Pde4dip</i>	21	3:97740393-97740400	-	mmu-miR-128-3p	7mer-m8
<i>Hipk1</i>	25	3:103742151-103742158	-	mmu-miR-128-3p	7mer-m8
<i>St7l</i>	12	3:104928523-104928530	+	mmu-miR-128-3p	7mer-m8
<i>Wnt2b</i>	17	3:104947024-104947031	-	mmu-miR-128-3p	7mer-m8
<i>Tmem64</i>	10	4:15283973-15283980	+	mmu-miR-128-3p	7mer-m8
<i>Mdn1</i>	17	4:32774812-32774819	+	mmu-miR-128-3p	7mer-m8
<i>Srsf12</i>	40	4:33231487-33231494	+	mmu-miR-128-3p	7mer-m8
<i>Rnf38</i>	12	4:44129460-44129467	-	mmu-miR-128-3p	7mer-m8
<i>Gabbr2</i>	29	4:46664066-46664073	-	mmu-miR-128-3p	7mer-m8
<i>Tmem246</i>	24	4:49585604-49585611	-	mmu-miR-128-3p	7mer-m8
<i>Rad23b</i>	16	4:55391428-55391435	+	mmu-miR-128-3p	7mer-m8
<i>Ptpn3</i>	24	4:57194184-57194191	-	mmu-miR-128-3p	7mer-m8
<i>Akap2</i>	19	4:57896023-57896030	+	mmu-miR-128-3p	7mer-m8
<i>Ugcg</i>	32	4:59221248-59221255	+	mmu-miR-128-3p	7mer-m8
<i>Rps6</i>	116	4:86854414-86854421	-	mmu-miR-128-3p	7mer-m8
<i>Focad</i>	22	4:88410830-88410837	+	mmu-miR-128-3p	7mer-m8
<i>Txndc12</i>	18	4:108861555-108861562	+	mmu-miR-128-3p	7mer-m8
<i>Elov1</i>	17	4:118432479-118432486	+	mmu-miR-128-3p	7mer-m8
<i>Meaf6</i>	15	4:125110506-125110513	+	mmu-miR-128-3p	7mer-m8
<i>AU040320</i>	11	4:126854037-126854044	+	mmu-miR-128-3p	7mer-m8
<i>Syf2</i>	21	4:134937454-134937461	+	mmu-miR-128-3p	7mer-m8
<i>Iffo2</i>	21	4:139617028-139617035	+	mmu-miR-128-3p	7mer-m8
<i>Iffo2</i>	21	4:139617051-139617058	+	mmu-miR-128-3p	7mer-m8
<i>Aldh4a1</i>	79	4:139649640-139649647	+	mmu-miR-128-3p	7mer-m8
<i>Kif1b</i>	34	4:149177191-149177198	-	mmu-miR-128-3p	7mer-m8
<i>Kif1b</i>	208	4:149180007-149180014	-	mmu-miR-128-3p	7mer-m8
<i>Rere</i>	17	4:150619828-150619835	+	mmu-miR-128-3p	7mer-m8
<i>Plch2</i>	15	4:154983206-154983213	-	mmu-miR-128-3p	7mer-m8
<i>Sdf4</i>	22	4:156011151-156011158	+	mmu-miR-128-3p	7mer-m8
<i>Adam22</i>	10	5:8075020-8075027	-	mmu-miR-128-3p	7mer-m8
<i>Rbm33</i>	42	5:28414970-28414977	+	mmu-miR-128-3p	7mer-m8
<i>Rbm33</i>	16	5:28418553-28418560	+	mmu-miR-128-3p	7mer-m8
<i>Sgcb</i>	22	5:73635099-73635106	-	mmu-miR-128-3p	7mer-m8
<i>Clock</i>	12	5:76216192-76216199	-	mmu-miR-128-3p	7mer-m8
<i>Rasgef1b</i>	31	5:99218105-99218112	-	mmu-miR-128-3p	7mer-m8
<i>Ulk1</i>	42	5:110784835-110784842	-	mmu-miR-128-3p	7mer-m8
<i>Asphd2</i>	26	5:112385640-112385647	-	mmu-miR-128-3p	7mer-m8
<i>Adrbk2</i>	13	5:112914937-112914944	-	mmu-miR-128-3p	7mer-m8
<i>Svop</i>	20	5:114028116-114028123	-	mmu-miR-128-3p	7mer-m8
<i>Rab35</i>	47	5:115647112-115647119	+	mmu-miR-128-3p	7mer-m8
<i>Rnft2</i>	29	5:118190717-118190724	-	mmu-miR-128-3p	7mer-m8
<i>Dtx1</i>	39	5:120680230-120680237	-	mmu-miR-128-3p	7mer-m8
<i>Bri3bp</i>	45	5:125454882-125454889	+	mmu-miR-128-3p	7mer-m8
<i>Ywhag</i>	44	5:135909577-135909584	-	mmu-miR-128-3p	7mer-m8
<i>Plod3</i>	41	5:136996291-136996298	+	mmu-miR-128-3p	7mer-m8
<i>Mcm7</i>	669	5:138165757-138165764	-	mmu-miR-128-3p	7mer-m8
<i>BC037034</i>	13	5:138260150-138260157	-	mmu-miR-128-3p	7mer-m8
<i>Cpsf4</i>	85	5:145181232-145181239	+	mmu-miR-128-3p	7mer-m8
<i>Ubl3</i>	236	5:148505457-148505464	-	mmu-miR-128-3p	7mer-m8
<i>Casd1</i>	13	6:4642645-4642652	+	mmu-miR-128-3p	7mer-m8
<i>Plxna4</i>	65	6:32150087-32150094	-	mmu-miR-128-3p	7mer-m8
<i>Slc37a3</i>	25	6:39336686-39336693	-	mmu-miR-128-3p	7mer-m8
<i>Wipf3</i>	30	6:54502574-54502581	+	mmu-miR-128-3p	7mer-m8
<i>Ppm1k</i>	23	6:57506703-57506710	-	mmu-miR-128-3p	7mer-m8
<i>Sec61a1</i>	84	6:88503664-88503671	-	mmu-miR-128-3p	7mer-m8
<i>Iqsec1</i>	22	6:90661733-90661740	-	mmu-miR-128-3p	7mer-m8
<i>Prickle2</i>	52	6:92373852-92373859	-	mmu-miR-128-3p	7mer-m8
<i>Ch1</i>	11	6:103731345-103731352	+	mmu-miR-128-3p	7mer-m8
<i>Srgap3</i>	31	6:112720805-112720812	-	mmu-miR-128-3p	7mer-m8
<i>Atp2b2</i>	30	6:113745187-113745194	-	mmu-miR-128-3p	7mer-m8
<i>Cecr6</i>	24	6:120489205-120489212	-	mmu-miR-128-3p	7mer-m8
<i>Bcl2l13</i>	32	6:120889868-120889875	+	mmu-miR-128-3p	7mer-m8
<i>Slc2a3</i>	19	6:122729896-122729903	-	mmu-miR-128-3p	7mer-m8

<i>Kcna1</i>	15	6:126637221-126637228	-	mmu-miR-128-3p	7mer-m8
<i>Tspan9</i>	49	6:127963503-127963510	-	mmu-miR-128-3p	7mer-m8
<i>Tspan9</i>	49	6:127963775-127963782	-	mmu-miR-128-3p	7mer-m8
<i>Crebl2</i>	18	6:134857022-134857029	+	mmu-miR-128-3p	7mer-m8
<i>Bhlhe41</i>	41	6:145862236-145862243	-	mmu-miR-128-3p	7mer-m8
<i>Ccdc9</i>	25	7:16275453-16275460	-	mmu-miR-128-3p	7mer-m8
<i>Sptbn4</i>	17	7:27357167-27357174	-	mmu-miR-128-3p	7mer-m8
<i>Sptbn4</i>	17	7:27357225-27357232	-	mmu-miR-128-3p	7mer-m8
<i>Emc10</i>	40	7:44490641-44490648	-	mmu-miR-128-3p	7mer-m8
<i>Grin2d</i>	20	7:45832418-45832425	-	mmu-miR-128-3p	7mer-m8
<i>Nav2</i>	54	7:49607627-49607634	+	mmu-miR-128-3p	7mer-m8
<i>Synm</i>	31	7:67730887-67730894	-	mmu-miR-128-3p	7mer-m8
<i>Tub</i>	46	7:109032949-109032956	+	mmu-miR-128-3p	7mer-m8
<i>Ampd3</i>	13	7:110811126-110811133	+	mmu-miR-128-3p	7mer-m8
<i>Coq7</i>	10	7:118525128-118525135	-	mmu-miR-128-3p	7mer-m8
<i>BC030336</i>	44	7:120731456-120731463	+	mmu-miR-128-3p	7mer-m8
<i>Tial1</i>	23	7:128442175-128442182	-	mmu-miR-128-3p	7mer-m8
<i>Rnh1</i>	68	7:141160385-141160392	-	mmu-miR-128-3p	7mer-m8
<i>Kcnq1ot1</i>	13	7:143290743-143290750	-	mmu-miR-128-3p	7mer-m8
<i>Golga7</i>	59	8:23241612-23241619	-	mmu-miR-128-3p	7mer-m8
<i>Whsc111</i>	48	8:25716972-25716979	+	mmu-miR-128-3p	7mer-m8
<i>Erlin2</i>	51	8:27037503-27037510	+	mmu-miR-128-3p	7mer-m8
<i>Tmem59l</i>	11	8:70484009-70484016	-	mmu-miR-128-3p	7mer-m8
<i>Slc27a1</i>	31	8:71586751-71586758	+	mmu-miR-128-3p	7mer-m8
<i>Nacc1</i>	57	8:84672431-84672438	-	mmu-miR-128-3p	7mer-m8
<i>Tnpo2</i>	27	8:85055606-85055613	+	mmu-miR-128-3p	7mer-m8
<i>Heatr3</i>	16	8:88171705-88171712	+	mmu-miR-128-3p	7mer-m8
<i>Gnao1</i>	11	8:93961401-93961408	+	mmu-miR-128-3p	7mer-m8
<i>Gnao1</i>	28	8:93967920-93967927	+	mmu-miR-128-3p	7mer-m8
<i>Cmtm4</i>	11	8:104349096-104349103	-	mmu-miR-128-3p	7mer-m8
<i>Smpd3</i>	13	8:106253385-106253392	-	mmu-miR-128-3p	7mer-m8
<i>Pdpr</i>	27	8:111135460-111135467	+	mmu-miR-128-3p	7mer-m8
<i>Hsdl1</i>	21	8:119562082-119562089	-	mmu-miR-128-3p	7mer-m8
<i>Fbxo31</i>	14	8:121549807-121549814	-	mmu-miR-128-3p	7mer-m8
<i>Slc7a5</i>	19	8:121882482-121882489	-	mmu-miR-128-3p	7mer-m8
<i>2310022B05Rik</i>	22	8:124637511-124637518	-	mmu-miR-128-3p	7mer-m8
<i>Slc35f3</i>	39	8:126395595-126395602	+	mmu-miR-128-3p	7mer-m8
<i>9230110C19Rik</i>	12	9:8022372-8022379	-	mmu-miR-128-3p	7mer-m8
<i>Fam76b</i>	21	9:13844380-13844387	+	mmu-miR-128-3p	7mer-m8
<i>Bbs9</i>	13	9:22887952-22887959	+	mmu-miR-128-3p	7mer-m8
<i>Aplp2</i>	114	9:31149881-31149888	-	mmu-miR-128-3p	7mer-m8
<i>Ddx6</i>	67	9:44636683-44636690	+	mmu-miR-128-3p	7mer-m8
<i>MII1</i>	20	9:44805694-44805701	-	mmu-miR-128-3p	7mer-m8
<i>MII1</i>	20	9:44805711-44805718	-	mmu-miR-128-3p	7mer-m8
<i>AI593442</i>	51	9:52677510-52677517	-	mmu-miR-128-3p	7mer-m8
<i>Cul5</i>	41	9:53617295-53617302	-	mmu-miR-128-3p	7mer-m8
<i>Tnfaip8l3</i>	414	9:54024718-54024725	-	mmu-miR-128-3p	7mer-m8
<i>Lingo1</i>	39	9:56618429-56618436	-	mmu-miR-128-3p	7mer-m8
<i>Parp6</i>	13	9:59650291-59650298	+	mmu-miR-128-3p	7mer-m8
<i>Myo9a</i>	10	9:59928216-59928223	+	mmu-miR-128-3p	7mer-m8
<i>Fem1b</i>	24	9:62795626-62795633	-	mmu-miR-128-3p	7mer-m8
<i>Polr2m</i>	27	9:71478917-71478924	-	mmu-miR-128-3p	7mer-m8
<i>Chst2</i>	11	9:95401099-95401106	-	mmu-miR-128-3p	7mer-m8
<i>Rab6b</i>	42	9:103183285-103183292	+	mmu-miR-128-3p	7mer-m8
<i>Rad54l2</i>	124	9:106688621-106688628	-	mmu-miR-128-3p	7mer-m8
<i>Myd88</i>	36	9:119336424-119336431	-	mmu-miR-128-3p	7mer-m8
<i>Prickle3</i>	13	X:7668335-7668342	+	mmu-miR-128-3p	7mer-m8
<i>Wdr13</i>	26	X:8128968-8128975	-	mmu-miR-128-3p	7mer-m8
<i>2900008C10Rik</i>	17	X:12134820-12134827	-	mmu-miR-128-3p	7mer-m8
<i>Prkx</i>	270	X:77761786-77761793	-	mmu-miR-128-3p	7mer-m8
<i>Pdk3</i>	88	X:93764280-93764287	-	mmu-miR-128-3p	7mer-m8
<i>C77370</i>	10	X:104081313-104081320	-	mmu-miR-128-3p	7mer-m8
<i>Drp2</i>	41	X:134456508-134456515	+	mmu-miR-128-3p	7mer-m8
<i>Iqsec2</i>	132	X:152223874-152223881	+	mmu-miR-128-3p	7mer-m8
<i>Paqr8</i>	33	1:20935723-20935730	+	mmu-miR-128-3p	7mer-A1
<i>Dst</i>	19	1:34307667-34307674	+	mmu-miR-128-3p	7mer-A1

2010300C02Rik	10	1:37612168-37612175	-	mmu-miR-128-3p	7mer-A1
Rnf149	15	1:39551474-39551481	-	mmu-miR-128-3p	7mer-A1
Nabp1	12	1:51471160-51471167	-	mmu-miR-128-3p	7mer-A1
Clk1	54	1:58417329-58417336	-	mmu-miR-128-3p	7mer-A1
Abi2	11	1:60479307-60479314	+	mmu-miR-128-3p	7mer-A1
Usp37	46	1:74437180-74437187	-	mmu-miR-128-3p	7mer-A1
Ncl	44	1:86347033-86347040	-	mmu-miR-128-3p	7mer-A1
6430706D22Rik	15	1:88264296-88264303	-	mmu-miR-128-3p	7mer-A1
Capn10	19	1:92947862-92947869	+	mmu-miR-128-3p	7mer-A1
Ppip5k2	14	1:97705391-97705398	-	mmu-miR-128-3p	7mer-A1
Ccnt2	16	1:127804415-127804422	+	mmu-miR-128-3p	7mer-A1
Slc41a1	10	1:131848484-131848491	+	mmu-miR-128-3p	7mer-A1
Cdk18	10	1:132113708-132113715	-	mmu-miR-128-3p	7mer-A1
Btg2	26	1:134076990-134076997	-	mmu-miR-128-3p	7mer-A1
Trove2	199	1:143757296-143757303	-	mmu-miR-128-3p	7mer-A1
1700025G04Rik	24	1:151886774-151886781	-	mmu-miR-128-3p	7mer-A1
Nmnat2	10	1:153117913-153117920	+	mmu-miR-128-3p	7mer-A1
Atf6	13	1:170707102-170707109	-	mmu-miR-128-3p	7mer-A1
Gm5069	10	1:180329929-180329936	-	mmu-miR-128-3p	7mer-A1
Camk1g	11	1:193346552-193346559	-	mmu-miR-128-3p	7mer-A1
Dusp18	30	11:3898461-3898468	+	mmu-miR-128-3p	7mer-A1
Cobl	10	11:12237223-12237230	-	mmu-miR-128-3p	7mer-A1
Cnrip1	31	11:17078686-17078693	+	mmu-miR-128-3p	7mer-A1
Ccdc104	19	11:29221770-29221777	-	mmu-miR-128-3p	7mer-A1
Gfpt2	36	11:49838045-49838052	+	mmu-miR-128-3p	7mer-A1
Rmnd5b	15	11:51624009-51624016	-	mmu-miR-128-3p	7mer-A1
Sowaha	83	11:53477583-53477590	-	mmu-miR-128-3p	7mer-A1
Sept8	17	11:53541967-53541974	+	mmu-miR-128-3p	7mer-A1
Map2k4	34	11:65690404-65690411	-	mmu-miR-128-3p	7mer-A1
Gas7	92	11:67684907-67684914	+	mmu-miR-128-3p	7mer-A1
Atp1b2	10	11:69600552-69600559	-	mmu-miR-128-3p	7mer-A1
Neurl4	27	11:69913645-69913652	+	mmu-miR-128-3p	7mer-A1
Supt6	19	11:78207142-78207149	-	mmu-miR-128-3p	7mer-A1
Sarm1	10	11:78471909-78471916	-	mmu-miR-128-3p	7mer-A1
Srsf1	12	11:88049849-88049856	+	mmu-miR-128-3p	7mer-A1
Ankrd40	20	11:94339724-94339731	+	mmu-miR-128-3p	7mer-A1
Kpnrb1	34	11:97160011-97160018	-	mmu-miR-128-3p	7mer-A1
Npepps	40	11:97206849-97206856	-	mmu-miR-128-3p	7mer-A1
Lasp1	52	11:97838303-97838310	+	mmu-miR-128-3p	7mer-A1
Fam134c	21	11:101098100-101098107	-	mmu-miR-128-3p	7mer-A1
Mpp2	25	11:102058436-102058443	-	mmu-miR-128-3p	7mer-A1
Rundc3a	36	11:102401640-102401647	+	mmu-miR-128-3p	7mer-A1
Gosr2	36	11:103679135-103679142	-	mmu-miR-128-3p	7mer-A1
Tlk2	29	11:105281562-105281569	+	mmu-miR-128-3p	7mer-A1
Tanc2	27	11:105925177-105925184	+	mmu-miR-128-3p	7mer-A1
Dcaf7	60	11:106055958-106055965	+	mmu-miR-128-3p	7mer-A1
Dcaf7	29	11:106058347-106058354	+	mmu-miR-128-3p	7mer-A1
Amz2	77	11:109437393-109437400	+	mmu-miR-128-3p	7mer-A1
Slc39a11	328	11:113244884-113244891	-	mmu-miR-128-3p	7mer-A1
Grb2	32	11:115644067-115644074	-	mmu-miR-128-3p	7mer-A1
Mfsd11	121	11:116874043-116874050	+	mmu-miR-128-3p	7mer-A1
Fn3krp	18	11:121430531-121430538	+	mmu-miR-128-3p	7mer-A1
Dnajc27	19	12:4107215-4107222	+	mmu-miR-128-3p	7mer-A1
Itsn2	24	12:4713784-4713791	+	mmu-miR-128-3p	7mer-A1
Id2	31	12:25094378-25094385	-	mmu-miR-128-3p	7mer-A1
Sstr1	61	12:58213950-58213957	+	mmu-miR-128-3p	7mer-A1
Sgpp1	17	12:75715357-75715364	-	mmu-miR-128-3p	7mer-A1
0610007P14Rik	22	12:85815708-85815715	-	mmu-miR-128-3p	7mer-A1
Calm1	11	12:100209816-100209823	+	mmu-miR-128-3p	7mer-A1
Otub2	27	12:103404586-103404593	+	mmu-miR-128-3p	7mer-A1
Hsp90aa1	13	12:110691395-110691402	-	mmu-miR-128-3p	7mer-A1
Traf3	20	12:111265210-111265217	+	mmu-miR-128-3p	7mer-A1
Aldh5a1	37	13:24907742-24907749	-	mmu-miR-128-3p	7mer-A1
Tmem170b	29	13:41640583-41640590	+	mmu-miR-128-3p	7mer-A1
Rasgrf2	12	13:91883673-91883680	-	mmu-miR-128-3p	7mer-A1
Sgtb	19	13:104140345-104140352	+	mmu-miR-128-3p	7mer-A1

<i>Fam149b</i>	13	14:20367949-20367956	+	mmu-miR-128-3p	7mer-A1
<i>Kcnma1</i>	15	14:23305789-23305796	-	mmu-miR-128-3p	7mer-A1
<i>Zcchc24</i>	41	14:25714962-25714969	-	mmu-miR-128-3p	7mer-A1
<i>Dennd6a</i>	13	14:26629587-26629594	+	mmu-miR-128-3p	7mer-A1
<i>Arhgef3</i>	11	14:27402963-27402970	+	mmu-miR-128-3p	7mer-A1
<i>Cacna2d3</i>	11	14:28905210-28905217	-	mmu-miR-128-3p	7mer-A1
<i>Kpna3</i>	41	14:61366157-61366164	-	mmu-miR-128-3p	7mer-A1
<i>Dock9</i>	38	14:121543365-121543372	-	mmu-miR-128-3p	7mer-A1
<i>March6</i>	13	15:31456791-31456798	-	mmu-miR-128-3p	7mer-A1
<i>Sdc2</i>	35	15:33034276-33034283	+	mmu-miR-128-3p	7mer-A1
<i>Rnf139</i>	26	15:58900246-58900253	+	mmu-miR-128-3p	7mer-A1
<i>Rnf139</i>	26	15:58900266-58900273	+	mmu-miR-128-3p	7mer-A1
<i>Hsf1</i>	18	15:76501050-76501057	+	mmu-miR-128-3p	7mer-A1
<i>Cacng2</i>	19	15:77993714-77993721	-	mmu-miR-128-3p	7mer-A1
<i>Rbx1</i>	36	15:81475620-81475627	+	mmu-miR-128-3p	7mer-A1
<i>Chadl</i>	24	15:81691531-81691538	-	mmu-miR-128-3p	7mer-A1
<i>Ldoc1l</i>	23	15:84554913-84554920	-	mmu-miR-128-3p	7mer-A1
<i>Mapk8ip2</i>	75	15:89463180-89463187	+	mmu-miR-128-3p	7mer-A1
<i>Shank3</i>	24	15:89559645-89559652	+	mmu-miR-128-3p	7mer-A1
<i>Arf3</i>	98	15:98739053-98739060	-	mmu-miR-128-3p	7mer-A1
<i>Tmbim6</i>	18	15:99409961-99409968	+	mmu-miR-128-3p	7mer-A1
<i>Zfp385a</i>	57	15:103314222-103314229	-	mmu-miR-128-3p	7mer-A1
<i>Ccdc50</i>	358	16:27451782-27451789	+	mmu-miR-128-3p	7mer-A1
<i>Pcyt1a</i>	43	16:32472323-32472330	+	mmu-miR-128-3p	7mer-A1
<i>Kalrn</i>	109	16:33970411-33970418	-	mmu-miR-128-3p	7mer-A1
<i>Stxbp5l</i>	29	16:37112982-37112989	-	mmu-miR-128-3p	7mer-A1
<i>Atp6v1a</i>	106	16:44087415-44087422	-	mmu-miR-128-3p	7mer-A1
<i>Bbx</i>	19	16:50196830-50196837	-	mmu-miR-128-3p	7mer-A1
<i>Cadm2</i>	11	16:66659461-66659468	-	mmu-miR-128-3p	7mer-A1
<i>Rps6ka2</i>	17	17:7303037-7303044	+	mmu-miR-128-3p	7mer-A1
<i>Smoc2</i>	17	17:14404406-14404413	+	mmu-miR-128-3p	7mer-A1
<i>Neurl1b</i>	19	17:26446149-26446156	+	mmu-miR-128-3p	7mer-A1
<i>Adamts10</i>	12	17:33553468-33553475	+	mmu-miR-128-3p	7mer-A1
<i>Rcan2</i>	88	17:44038680-44038687	+	mmu-miR-128-3p	7mer-A1
<i>Sos1</i>	19	17:80396747-80396754	-	mmu-miR-128-3p	7mer-A1
<i>Zfp36l2</i>	56	17:84184464-84184471	-	mmu-miR-128-3p	7mer-A1
<i>Ppm1b</i>	44	17:85024643-85024650	+	mmu-miR-128-3p	7mer-A1
<i>Crem</i>	17	18:3267953-3267960	-	mmu-miR-128-3p	7mer-A1
<i>Npc1</i>	16	18:12190053-12190060	-	mmu-miR-128-3p	7mer-A1
<i>Slc25a46</i>	19	18:31581732-31581739	-	mmu-miR-128-3p	7mer-A1
<i>Nrg2</i>	22	18:36017473-36017480	-	mmu-miR-128-3p	7mer-A1
<i>Onecut2</i>	174	18:64388010-64388017	+	mmu-miR-128-3p	7mer-A1
<i>Nedd4l</i>	134	18:65217740-65217747	+	mmu-miR-128-3p	7mer-A1
<i>Neto1</i>	26	18:86500939-86500946	+	mmu-miR-128-3p	7mer-A1
<i>Al846148</i>	11	19:7356560-7356567	-	mmu-miR-128-3p	7mer-A1
<i>Pla2g16</i>	17	19:7587339-7587346	+	mmu-miR-128-3p	7mer-A1
<i>Slc1a1</i>	16	19:28912744-28912751	+	mmu-miR-128-3p	7mer-A1
<i>Cpeb3</i>	35	19:37022210-37022217	-	mmu-miR-128-3p	7mer-A1
<i>March5</i>	23	19:37221887-37221894	+	mmu-miR-128-3p	7mer-A1
<i>Ccnj</i>	10	19:40848377-40848384	+	mmu-miR-128-3p	7mer-A1
<i>Fam171a1</i>	12	2:3226871-3226878	+	mmu-miR-128-3p	7mer-A1
<i>Prpf18</i>	21	2:4621672-4621679	-	mmu-miR-128-3p	7mer-A1
<i>Il15ra</i>	10	2:11733204-11733211	+	mmu-miR-128-3p	7mer-A1
<i>Thns1l</i>	35	2:21214205-21214212	+	mmu-miR-128-3p	7mer-A1
<i>Nsmf</i>	78	2:25062666-25062673	+	mmu-miR-128-3p	7mer-A1
<i>Dnlz</i>	31	2:26348441-26348448	-	mmu-miR-128-3p	7mer-A1
<i>Cacfd1</i>	17	2:27018971-27018978	+	mmu-miR-128-3p	7mer-A1
<i>Rxra</i>	11	2:27762799-27762806	+	mmu-miR-128-3p	7mer-A1
<i>6530402F18Rik</i>	11	2:29247774-29247781	-	mmu-miR-128-3p	7mer-A1
<i>Fam78a</i>	10	2:32066994-32067001	-	mmu-miR-128-3p	7mer-A1
<i>Rabgap1</i>	165	2:37565543-37565550	+	mmu-miR-128-3p	7mer-A1
<i>Acvr1c</i>	108	2:58269618-58269625	-	mmu-miR-128-3p	7mer-A1
<i>Acp2</i>	43	2:91211467-91211474	+	mmu-miR-128-3p	7mer-A1
<i>Chst1</i>	30	2:92615001-92615008	+	mmu-miR-128-3p	7mer-A1
<i>Slc1a2</i>	67	2:102782828-102782835	+	mmu-miR-128-3p	7mer-A1
<i>Slc1a2</i>	16	2:102787893-102787900	+	mmu-miR-128-3p	7mer-A1

D430041D05Rik	45	2:104145702-104145709	-	mmu-miR-128-3p	7mer-A1
Pak6	28	2:118697144-118697151	+	mmu-miR-128-3p	7mer-A1
Slc30a4	31	2:122682949-122682956	-	mmu-miR-128-3p	7mer-A1
Prosapip1	27	2:130633203-130633210	-	mmu-miR-128-3p	7mer-A1
Tmx4	50	2:134594963-134594970	-	mmu-miR-128-3p	7mer-A1
Snap25	12	2:136781549-136781556	+	mmu-miR-128-3p	7mer-A1
Snap25	27	2:136782301-136782308	+	mmu-miR-128-3p	7mer-A1
Btbd3	24	2:138286673-138286680	+	mmu-miR-128-3p	7mer-A1
Flrt3	44	2:140659425-140659432	-	mmu-miR-128-3p	7mer-A1
Dzank1	65	2:144471679-144471686	-	mmu-miR-128-3p	7mer-A1
Epb4.1I1	23	2:156540756-156540763	+	mmu-miR-128-3p	7mer-A1
Epb4.1I1	23	2:156540859-156540866	+	mmu-miR-128-3p	7mer-A1
Zhx3	20	2:160771593-160771600	-	mmu-miR-128-3p	7mer-A1
Ube2v1	11	2:167608806-167608813	-	mmu-miR-128-3p	7mer-A1
Bcas1	21	2:170347088-170347095	-	mmu-miR-128-3p	7mer-A1
Dclk1	10	3:55538320-55538327	+	mmu-miR-128-3p	7mer-A1
Ssr3	14	3:65381165-65381172	-	mmu-miR-128-3p	7mer-A1
1110032F04Rik	17	3:68870980-68870987	+	mmu-miR-128-3p	7mer-A1
Ppm1l	113	3:69556010-69556017	+	mmu-miR-128-3p	7mer-A1
Serpini1	12	3:75641199-75641206	+	mmu-miR-128-3p	7mer-A1
HaplN2	24	3:88021222-88021229	-	mmu-miR-128-3p	7mer-A1
Prune	10	3:95254650-95254657	-	mmu-miR-128-3p	7mer-A1
Dram2	22	3:106573757-106573764	+	mmu-miR-128-3p	7mer-A1
Fubp1	18	3:152236647-152236654	+	mmu-miR-128-3p	7mer-A1
2610301B20Rik	29	4:10898200-10898207	+	mmu-miR-128-3p	7mer-A1
Frrs1l	10	4:56962709-56962716	-	mmu-miR-128-3p	7mer-A1
Palm2	10	4:57710272-57710279	+	mmu-miR-128-3p	7mer-A1
Zkscan16	18	4:58959246-58959253	+	mmu-miR-128-3p	7mer-A1
Zdhhc21	50	4:82798986-82798993	-	mmu-miR-128-3p	7mer-A1
Zdhhc21	50	4:82799032-82799039	-	mmu-miR-128-3p	7mer-A1
E130102H24Rik	92	4:101346964-101346971	-	mmu-miR-128-3p	7mer-A1
Sgip1	10	4:102971227-102971234	+	mmu-miR-128-3p	7mer-A1
B4galt2	16	4:117877796-117877803	-	mmu-miR-128-3p	7mer-A1
Ak2	12	4:129010824-129010831	+	mmu-miR-128-3p	7mer-A1
Nkain1	28	4:130531491-130531498	-	mmu-miR-128-3p	7mer-A1
Dnajc16	26	4:141762457-141762464	-	mmu-miR-128-3p	7mer-A1
Efh2d	40	4:141858742-141858749	-	mmu-miR-128-3p	7mer-A1
Camta1	118	4:151060070-151060077	-	mmu-miR-128-3p	7mer-A1
A330021E22Rik	11	5:5580884-5580891	-	mmu-miR-128-3p	7mer-A1
Cacna2d1	36	5:16371301-16371308	+	mmu-miR-128-3p	7mer-A1
Nat8l	39	5:34005735-34005742	+	mmu-miR-128-3p	7mer-A1
Add1	16	5:34631595-34631602	+	mmu-miR-128-3p	7mer-A1
Sgcb	24	5:73633851-73633858	-	mmu-miR-128-3p	7mer-A1
Clock	385	5:76213911-76213918	-	mmu-miR-128-3p	7mer-A1
Cox18	65	5:90222696-90222703	-	mmu-miR-128-3p	7mer-A1
Rchy1	33	5:91957890-91957897	-	mmu-miR-128-3p	7mer-A1
Prkg2	29	5:98931955-98931962	-	mmu-miR-128-3p	7mer-A1
Srrd	16	5:112337583-112337590	-	mmu-miR-128-3p	7mer-A1
Setd8	14	5:124462153-124462160	+	mmu-miR-128-3p	7mer-A1
Limk1	23	5:134656204-134656211	-	mmu-miR-128-3p	7mer-A1
Pom121	12	5:135376150-135376157	-	mmu-miR-128-3p	7mer-A1
Cox19	11	5:139337144-139337151	-	mmu-miR-128-3p	7mer-A1
Gna12	40	5:140760331-140760338	-	mmu-miR-128-3p	7mer-A1
Plxna4	11	6:32149954-32149961	-	mmu-miR-128-3p	7mer-A1
Plxna4	65	6:32150055-32150062	-	mmu-miR-128-3p	7mer-A1
Ggct	24	6:54984761-54984768	-	mmu-miR-128-3p	7mer-A1
Ppm1k	23	6:57506563-57506570	-	mmu-miR-128-3p	7mer-A1
Rmnd5a	22	6:71389257-71389264	-	mmu-miR-128-3p	7mer-A1
Tgoln1	22	6:72612030-72612037	-	mmu-miR-128-3p	7mer-A1
Tex261	20	6:83770546-83770553	-	mmu-miR-128-3p	7mer-A1
Rpn1	29	6:88103951-88103958	+	mmu-miR-128-3p	7mer-A1
Prickle2	15	6:92375029-92375036	-	mmu-miR-128-3p	7mer-A1
Setd5	23	6:113152793-113152800	+	mmu-miR-128-3p	7mer-A1
Slc6a1	14	6:114317164-114317171	+	mmu-miR-128-3p	7mer-A1
Slc6a1	14	6:114317173-114317180	+	mmu-miR-128-3p	7mer-A1
Hnrnpf	5730	6:117925525-117925532	+	mmu-miR-128-3p	7mer-A1

<i>Cecr6</i>	102	6:120489944-120489951	-	mmu-miR-128-3p	7mer-A1
<i>Itpr2</i>	22	6:146108833-146108840	-	mmu-miR-128-3p	7mer-A1
<i>Itpr2</i>	22	6:146108906-146108913	-	mmu-miR-128-3p	7mer-A1
<i>Gm4636</i>	25	7:27988507-27988514	-	mmu-miR-128-3p	7mer-A1
<i>Grin2d</i>	20	7:45832217-45832224	-	mmu-miR-128-3p	7mer-A1
<i>Grin2d</i>	20	7:45832273-45832280	-	mmu-miR-128-3p	7mer-A1
<i>Grin2d</i>	20	7:45832322-45832329	-	mmu-miR-128-3p	7mer-A1
<i>Grin2d</i>	20	7:45832343-45832350	-	mmu-miR-128-3p	7mer-A1
<i>Gabrb3</i>	19	7:57826952-57826959	+	mmu-miR-128-3p	7mer-A1
<i>Arrdc4</i>	13	7:68738353-68738360	-	mmu-miR-128-3p	7mer-A1
<i>Arrb1</i>	61	7:99601647-99601654	+	mmu-miR-128-3p	7mer-A1
<i>Wee1</i>	145	7:110142153-110142160	+	mmu-miR-128-3p	7mer-A1
<i>Prkcb</i>	34	7:122631145-122631152	+	mmu-miR-128-3p	7mer-A1
<i>Tnrc6a</i>	775	7:123192971-123192978	+	mmu-miR-128-3p	7mer-A1
<i>Gsg1l</i>	38	7:125880348-125880355	-	mmu-miR-128-3p	7mer-A1
<i>Sbk1</i>	35	7:126294782-126294789	+	mmu-miR-128-3p	7mer-A1
<i>Fank1</i>	43	7:133880704-133880711	+	mmu-miR-128-3p	7mer-A1
<i>Sprn</i>	20	7:140151119-140151126	-	mmu-miR-128-3p	7mer-A1
<i>Brsk2</i>	20	7:142004199-142004206	+	mmu-miR-128-3p	7mer-A1
<i>Zfp958</i>	31	8:4630552-4630559	+	mmu-miR-128-3p	7mer-A1
<i>Ankrd10</i>	36	8:11615339-11615346	-	mmu-miR-128-3p	7mer-A1
<i>Atp11a</i>	28	8:12866075-12866082	+	mmu-miR-128-3p	7mer-A1
<i>Zmat4</i>	42	8:24060782-24060789	+	mmu-miR-128-3p	7mer-A1
<i>Cnot7</i>	12	8:40492842-40492849	-	mmu-miR-128-3p	7mer-A1
<i>Galnt7</i>	16	8:57525957-57525964	-	mmu-miR-128-3p	7mer-A1
<i>Cbr4</i>	10	8:61503225-61503232	+	mmu-miR-128-3p	7mer-A1
<i>Mast3</i>	12	8:70778352-70778359	-	mmu-miR-128-3p	7mer-A1
<i>Cacna1a</i>	21	8:84640181-84640188	+	mmu-miR-128-3p	7mer-A1
<i>Neto2</i>	20	8:85639294-85639301	-	mmu-miR-128-3p	7mer-A1
<i>N4bp1</i>	11	8:86841237-86841244	-	mmu-miR-128-3p	7mer-A1
<i>Cyld</i>	19	8:88749487-88749494	+	mmu-miR-128-3p	7mer-A1
<i>Rpgrip11</i>	13	8:91219717-91219724	-	mmu-miR-128-3p	7mer-A1
<i>Cfbf</i>	19	8:105216049-105216056	+	mmu-miR-128-3p	7mer-A1
<i>Ctcf</i>	25	8:105681843-105681850	+	mmu-miR-128-3p	7mer-A1
<i>Nfat5</i>	45	8:107374456-107374463	+	mmu-miR-128-3p	7mer-A1
<i>Phlpp2</i>	57	8:109941464-109941471	+	mmu-miR-128-3p	7mer-A1
<i>Cbfa2t3</i>	11	8:122630143-122630150	-	mmu-miR-128-3p	7mer-A1
<i>Ankrd11</i>	18	8:122896027-122896034	-	mmu-miR-128-3p	7mer-A1
<i>Pgbd5</i>	18	8:124369920-124369927	-	mmu-miR-128-3p	7mer-A1
<i>Gucy1a2</i>	525	9:3902759-3902766	+	mmu-miR-128-3p	7mer-A1
<i>Arhgap42</i>	35	9:8994903-8994910	-	mmu-miR-128-3p	7mer-A1
<i>Ubash3b</i>	15	9:41014133-41014140	-	mmu-miR-128-3p	7mer-A1
<i>Ift46</i>	20	9:44792718-44792725	+	mmu-miR-128-3p	7mer-A1
<i>Scn2b</i>	31	9:45129075-45129082	+	mmu-miR-128-3p	7mer-A1
<i>Cadm1</i>	37	9:47851139-47851146	+	mmu-miR-128-3p	7mer-A1
<i>Exph5</i>	35	9:53381106-53381113	+	mmu-miR-128-3p	7mer-A1
<i>Slc35f2</i>	13	9:53817445-53817452	+	mmu-miR-128-3p	7mer-A1
<i>Dmxl2</i>	11	9:54365940-54365947	-	mmu-miR-128-3p	7mer-A1
<i>Sema7a</i>	39	9:57962654-57962661	+	mmu-miR-128-3p	7mer-A1
<i>Chst2</i>	11	9:95401178-95401185	-	mmu-miR-128-3p	7mer-A1
<i>Dbr1</i>	18	9:99584035-99584042	+	mmu-miR-128-3p	7mer-A1
<i>Stag1</i>	37	9:100956615-100956622	+	mmu-miR-128-3p	7mer-A1
<i>Rad54l2</i>	124	9:106688717-106688724	-	mmu-miR-128-3p	7mer-A1
<i>Rbm5</i>	22	9:107740776-107740783	-	mmu-miR-128-3p	7mer-A1
<i>Ubp1</i>	22	9:113975477-113975484	+	mmu-miR-128-3p	7mer-A1
<i>Wdr13</i>	18	X:8125611-8125618	-	mmu-miR-128-3p	7mer-A1
6720401G13Rik	13	X:50569885-50569892	-	mmu-miR-128-3p	7mer-A1
<i>Vbp1</i>	225	X:75534239-75534246	+	mmu-miR-128-3p	7mer-A1
<i>Dlg3</i>	59	X:100818117-100818124	+	mmu-miR-128-3p	7mer-A1
<i>Zdhhc15</i>	32	X:104540593-104540600	-	mmu-miR-128-3p	7mer-A1
<i>Ngfrap1</i>	75	X:136271692-136271699	+	mmu-miR-128-3p	7mer-A1
<i>Txlng</i>	12	X:162779114-162779121	-	mmu-miR-128-3p	7mer-A1
<i>Lmbrd1</i>	14	1:24762932-24762938	+	mmu-miR-128-3p	6mer
<i>Phf3</i>	18	1:30803736-30803742	-	mmu-miR-128-3p	6mer
<i>Amer3</i>	20	1:34590376-34590382	+	mmu-miR-128-3p	6mer
<i>Fam168b</i>	14	1:34813597-34813603	-	mmu-miR-128-3p	6mer

<i>Fam168b</i>	89	1:34814145-34814151	-	mmu-miR-128-3p	6mer
<i>Plekhb2</i>	39	1:34877446-34877452	+	mmu-miR-128-3p	6mer
<i>Kansl3</i>	45	1:36336857-36336863	-	mmu-miR-128-3p	6mer
<i>Rnf149</i>	16	1:39552024-39552030	-	mmu-miR-128-3p	6mer
<i>Creg2</i>	35	1:39621883-39621889	-	mmu-miR-128-3p	6mer
<i>Pou3f3</i>	18	1:42699056-42699062	+	mmu-miR-128-3p	6mer
<i>Nck2</i>	19	1:43569910-43569916	+	mmu-miR-128-3p	6mer
<i>Gls</i>	10	1:52165882-52165888	-	mmu-miR-128-3p	6mer
<i>Pgap1</i>	15	1:54474404-54474410	-	mmu-miR-128-3p	6mer
<i>Pgap1</i>	15	1:54474456-54474462	-	mmu-miR-128-3p	6mer
<i>Ino80d</i>	12	1:63056931-63056937	-	mmu-miR-128-3p	6mer
<i>Map2</i>	24	1:66441070-66441076	+	mmu-miR-128-3p	6mer
<i>Epha4</i>	14	1:77367722-77367728	-	mmu-miR-128-3p	6mer
<i>Kif1a</i>	16	1:93018085-93018091	-	mmu-miR-128-3p	6mer
<i>Arl8a</i>	33	1:135155272-135155278	+	mmu-miR-128-3p	6mer
<i>Nav1</i>	10	1:135439936-135439942	-	mmu-miR-128-3p	6mer
<i>Camsap2</i>	24	1:136269629-136269635	-	mmu-miR-128-3p	6mer
<i>Rgs2</i>	15	1:144001226-144001232	-	mmu-miR-128-3p	6mer
<i>Acbd6</i>	12	1:155687305-155687311	+	mmu-miR-128-3p	6mer
<i>Astn1</i>	67	1:158690906-158690912	+	mmu-miR-128-3p	6mer
<i>Vamp4</i>	21	1:162598134-162598140	+	mmu-miR-128-3p	6mer
<i>Sft2d2</i>	10	1:165176626-165176632	-	mmu-miR-128-3p	6mer
<i>Sft2d2</i>	22	1:165177787-165177793	-	mmu-miR-128-3p	6mer
<i>Sft2d2</i>	22	1:165177825-165177831	-	mmu-miR-128-3p	6mer
<i>Adamts4</i>	19	1:171260905-171260911	+	mmu-miR-128-3p	6mer
<i>Pfdn2</i>	17	1:171359006-171359012	+	mmu-miR-128-3p	6mer
<i>Pvrl4</i>	19	1:171387261-171387267	+	mmu-miR-128-3p	6mer
<i>Pea15a</i>	49	1:172197502-172197508	-	mmu-miR-128-3p	6mer
<i>Kcnj10</i>	60	1:172371908-172371914	+	mmu-miR-128-3p	6mer
<i>Akt3</i>	56	1:177021730-177021736	-	mmu-miR-128-3p	6mer
<i>Zbtb18</i>	40	1:177449330-177449336	+	mmu-miR-128-3p	6mer
<i>Zbtb18</i>	19	1:177450056-177450062	+	mmu-miR-128-3p	6mer
<i>Srp9</i>	11	1:182131941-182131947	+	mmu-miR-128-3p	6mer
<i>Capn2</i>	37	1:182467401-182467407	-	mmu-miR-128-3p	6mer
<i>Susd4</i>	52	1:182895373-182895379	+	mmu-miR-128-3p	6mer
<i>Slc30a1</i>	24	1:191911489-191911495	+	mmu-miR-128-3p	6mer
<i>Pik3ip1</i>	10	11:3342820-3342826	+	mmu-miR-128-3p	6mer
<i>Tug1</i>	34	11:3639866-3639872	-	mmu-miR-128-3p	6mer
<i>Tug1</i>	69	11:3646960-3646966	-	mmu-miR-128-3p	6mer
<i>Sf3a1</i>	12	11:4180541-4180547	+	mmu-miR-128-3p	6mer
<i>Adcy1</i>	74	11:7173883-7173889	+	mmu-miR-128-3p	6mer
<i>Adcy1</i>	74	11:7173934-7173940	+	mmu-miR-128-3p	6mer
<i>Adcy1</i>	28	11:7177727-7177733	+	mmu-miR-128-3p	6mer
<i>Clint1</i>	33	11:45909233-45909239	+	mmu-miR-128-3p	6mer
<i>Gfpt2</i>	36	11:49838011-49838017	+	mmu-miR-128-3p	6mer
<i>Phf15</i>	11	11:51814306-51814312	-	mmu-miR-128-3p	6mer
<i>Cdc42se2</i>	12	11:54718817-54718823	-	mmu-miR-128-3p	6mer
<i>Slc36a1</i>	11	11:55235771-55235777	+	mmu-miR-128-3p	6mer
<i>G3bp1</i>	20	11:55500422-55500428	+	mmu-miR-128-3p	6mer
<i>Cnot8</i>	23	11:58118325-58118331	+	mmu-miR-128-3p	6mer
<i>Zfp672</i>	13	11:58315379-58315385	-	mmu-miR-128-3p	6mer
<i>Wnt9a</i>	12	11:59333427-59333433	+	mmu-miR-128-3p	6mer
<i>Tom1l2</i>	82	11:60228342-60228348	-	mmu-miR-128-3p	6mer
<i>Tom1l2</i>	11	11:60229630-60229636	-	mmu-miR-128-3p	6mer
<i>Smcr8</i>	14	11:60784514-60784520	+	mmu-miR-128-3p	6mer
<i>Ulk2</i>	15	11:61777783-61777789	-	mmu-miR-128-3p	6mer
<i>Ankfy1</i>	10	11:72768388-72768394	+	mmu-miR-128-3p	6mer
<i>Ctns</i>	27	11:73184335-73184341	-	mmu-miR-128-3p	6mer
<i>Ywhae</i>	34	11:75765221-75765227	+	mmu-miR-128-3p	6mer
<i>Glod4</i>	28	11:76221052-76221058	-	mmu-miR-128-3p	6mer
<i>Sarm1</i>	11	11:78471518-78471524	-	mmu-miR-128-3p	6mer
<i>Sarm1</i>	10	11:78471871-78471877	-	mmu-miR-128-3p	6mer
<i>Poldip2</i>	31	11:78522492-78522498	+	mmu-miR-128-3p	6mer
<i>Nlk</i>	54	11:78568915-78568921	-	mmu-miR-128-3p	6mer
<i>Cdk5r1</i>	12	11:80479508-80479514	+	mmu-miR-128-3p	6mer
<i>Cdk5r1</i>	42	11:80480428-80480434	+	mmu-miR-128-3p	6mer

<i>Cdk5r1</i>	38	11:80481146-80481152	+	mmu-miR-128-3p	6mer
<i>Dusp14</i>	12	11:84047964-84047970	-	mmu-miR-128-3p	6mer
<i>Appbp2</i>	46	11:85190796-85190802	-	mmu-miR-128-3p	6mer
<i>Med13</i>	29	11:86269669-86269675	-	mmu-miR-128-3p	6mer
<i>Spag9</i>	45	11:94124832-94124838	+	mmu-miR-128-3p	6mer
<i>Milt6</i>	23	11:97685167-97685173	+	mmu-miR-128-3p	6mer
<i>Cwc25</i>	20	11:97747118-97747124	-	mmu-miR-128-3p	6mer
<i>Ormdl3</i>	15	11:98582425-98582431	-	mmu-miR-128-3p	6mer
<i>Thra</i>	29	11:98765595-98765601	+	mmu-miR-128-3p	6mer
<i>Jup</i>	21	11:100371408-100371414	-	mmu-miR-128-3p	6mer
<i>Atp6v0a1</i>	105	11:101062611-101062617	+	mmu-miR-128-3p	6mer
<i>Becn1</i>	53	11:101288319-101288325	-	mmu-miR-128-3p	6mer
<i>Ubtf</i>	11	11:102305084-102305090	-	mmu-miR-128-3p	6mer
<i>Rundc3a</i>	36	11:102401618-102401624	+	mmu-miR-128-3p	6mer
<i>Arhgap27</i>	13	11:103332857-103332863	-	mmu-miR-128-3p	6mer
<i>Arf2</i>	109	11:103984748-103984754	+	mmu-miR-128-3p	6mer
<i>Limd2</i>	32	11:106158473-106158479	-	mmu-miR-128-3p	6mer
<i>Ccdc47</i>	42	11:106199695-106199701	-	mmu-miR-128-3p	6mer
<i>Icam2</i>	13	11:106377722-106377728	-	mmu-miR-128-3p	6mer
<i>Gna13</i>	22	11:109397425-109397431	+	mmu-miR-128-3p	6mer
<i>Cdc42ep4</i>	32	11:113727683-113727689	-	mmu-miR-128-3p	6mer
<i>Ttyh2</i>	31	11:114719990-114719996	+	mmu-miR-128-3p	6mer
<i>Gga3</i>	34	11:115585508-115585514	-	mmu-miR-128-3p	6mer
<i>Grb2</i>	32	11:115644039-115644045	-	mmu-miR-128-3p	6mer
<i>Tnrc6c</i>	12	11:117761665-117761671	+	mmu-miR-128-3p	6mer
<i>Tnrc6c</i>	80	11:117762065-117762071	+	mmu-miR-128-3p	6mer
<i>Cyth1</i>	12	11:118165449-118165455	-	mmu-miR-128-3p	6mer
<i>Cbx8</i>	21	11:119038383-119038389	-	mmu-miR-128-3p	6mer
<i>Nploc4</i>	10	11:120381211-120381217	-	mmu-miR-128-3p	6mer
<i>Alyref</i>	16	11:120594769-120594775	-	mmu-miR-128-3p	6mer
<i>Gps1</i>	10	11:120788849-120788855	+	mmu-miR-128-3p	6mer
<i>Csnk1d</i>	12	11:120963921-120963927	-	mmu-miR-128-3p	6mer
<i>Rab10</i>	10	12:3246435-3246441	-	mmu-miR-128-3p	6mer
<i>Klhl29</i>	20	12:5080598-5080604	-	mmu-miR-128-3p	6mer
<i>Pum2</i>	47	12:8749979-8749985	+	mmu-miR-128-3p	6mer
<i>Myt1l</i>	21	12:29921255-29921261	+	mmu-miR-128-3p	6mer
<i>Nova1</i>	16	12:46698044-46698050	-	mmu-miR-128-3p	6mer
<i>Clec14a</i>	14	12:58267313-58267319	-	mmu-miR-128-3p	6mer
<i>Ppp2r5e</i>	35	12:75453777-75453783	-	mmu-miR-128-3p	6mer
<i>Sgpp1</i>	17	12:75715398-75715404	-	mmu-miR-128-3p	6mer
<i>Nek9</i>	30	12:85300024-85300030	-	mmu-miR-128-3p	6mer
<i>Calm1</i>	11	12:100209823-100209829	+	mmu-miR-128-3p	6mer
<i>Clmn</i>	50	12:104771552-104771558	-	mmu-miR-128-3p	6mer
<i>Gm266</i>	15	12:111484708-111484714	-	mmu-miR-128-3p	6mer
<i>Jag2</i>	449	12:112908048-112908054	-	mmu-miR-128-3p	6mer
<i>Jag2</i>	58	12:112908372-112908378	-	mmu-miR-128-3p	6mer
<i>Vipr2</i>	17	12:116145160-116145166	+	mmu-miR-128-3p	6mer
<i>Rapgef5</i>	31	12:117756479-117756485	+	mmu-miR-128-3p	6mer
<i>Zmynd11</i>	34	13:9685123-9685129	-	mmu-miR-128-3p	6mer
<i>Chrm3</i>	18	13:9876071-9876077	-	mmu-miR-128-3p	6mer
<i>Ero1lb</i>	22	13:12608800-12608806	+	mmu-miR-128-3p	6mer
<i>Ero1lb</i>	22	13:12608807-12608813	+	mmu-miR-128-3p	6mer
<i>Gng4</i>	10	13:13826317-13826323	+	mmu-miR-128-3p	6mer
<i>BC005537</i>	60	13:24812968-24812974	+	mmu-miR-128-3p	6mer
<i>Nrsn1</i>	35	13:25252241-25252247	-	mmu-miR-128-3p	6mer
<i>Sox4</i>	11	13:28950667-28950673	-	mmu-miR-128-3p	6mer
<i>Ssr1</i>	65	13:37974476-37974482	-	mmu-miR-128-3p	6mer
<i>Ssr1</i>	36	13:37979504-37979510	-	mmu-miR-128-3p	6mer
<i>Gcnt2</i>	12	13:40960812-40960818	+	mmu-miR-128-3p	6mer
<i>Ccdc90a</i>	11	13:43541522-43541528	-	mmu-miR-128-3p	6mer
<i>Nup153</i>	25	13:46680211-46680217	-	mmu-miR-128-3p	6mer
<i>Bicd2</i>	33	13:49386225-49386231	+	mmu-miR-128-3p	6mer
<i>Rnf44</i>	17	13:54680080-54680086	-	mmu-miR-128-3p	6mer
<i>Nsd1</i>	30	13:55317655-55317661	+	mmu-miR-128-3p	6mer
<i>Isca1</i>	10	13:59756371-59756377	-	mmu-miR-128-3p	6mer
<i>Tppp</i>	51	13:74032521-74032527	+	mmu-miR-128-3p	6mer

<i>Arrdc3</i>	47	13:80894063-80894069	+	mmu-miR-128-3p	6mer
<i>Edil3</i>	20	13:89319884-89319890	+	mmu-miR-128-3p	6mer
<i>Rasgrf2</i>	14	13:91881692-91881698	-	mmu-miR-128-3p	6mer
<i>Serinc5</i>	23	13:92710709-92710715	+	mmu-miR-128-3p	6mer
<i>Mtx3</i>	20	13:92854069-92854075	+	mmu-miR-128-3p	6mer
<i>Homer1</i>	29	13:93404778-93404784	+	mmu-miR-128-3p	6mer
<i>Lhfpl2</i>	11	13:94195131-94195137	+	mmu-miR-128-3p	6mer
<i>Wdr41</i>	34	13:95023572-95023578	+	mmu-miR-128-3p	6mer
<i>Enc1</i>	11	13:97252523-97252529	+	mmu-miR-128-3p	6mer
<i>Kif2a</i>	21	13:106961559-106961565	-	mmu-miR-128-3p	6mer
<i>Il6st</i>	25	13:112505633-112505639	+	mmu-miR-128-3p	6mer
<i>Ube2e2</i>	14	14:18573635-18573641	-	mmu-miR-128-3p	6mer
<i>Gng2</i>	25	14:19874843-19874849	-	mmu-miR-128-3p	6mer
<i>Fut11</i>	22	14:20698398-20698404	+	mmu-miR-128-3p	6mer
<i>Zmiz1</i>	46	14:25665243-25665249	+	mmu-miR-128-3p	6mer
<i>Anxa11</i>	21	14:25886550-25886556	+	mmu-miR-128-3p	6mer
<i>Cacna2d3</i>	11	14:28905139-28905145	-	mmu-miR-128-3p	6mer
<i>Cacna1d</i>	15	14:30040106-30040112	-	mmu-miR-128-3p	6mer
<i>Sfmbt1</i>	15	14:30818269-30818275	+	mmu-miR-128-3p	6mer
<i>Gpr137c</i>	39	14:45280734-45280740	+	mmu-miR-128-3p	6mer
<i>Gmfb</i>	16	14:46810996-46811002	-	mmu-miR-128-3p	6mer
<i>Naa30</i>	29	14:49187671-49187677	+	mmu-miR-128-3p	6mer
<i>Jph4</i>	567	14:55107155-55107161	-	mmu-miR-128-3p	6mer
<i>Zdhhc20</i>	16	14:57835565-57835571	-	mmu-miR-128-3p	6mer
<i>Dleu2</i>	297	14:61631900-61631906	-	mmu-miR-128-3p	6mer
<i>Dleu2</i>	297	14:61632045-61632051	-	mmu-miR-128-3p	6mer
<i>Lrch1</i>	55	14:74755202-74755208	-	mmu-miR-128-3p	6mer
<i>Slitrk1</i>	17	14:108910983-108910989	-	mmu-miR-128-3p	6mer
<i>Hs6st3</i>	15	14:119870750-119870756	+	mmu-miR-128-3p	6mer
<i>Myo10</i>	20	15:25812558-25812564	+	mmu-miR-128-3p	6mer
<i>Sdc2</i>	13	15:33034582-33034588	+	mmu-miR-128-3p	6mer
<i>Mtdh</i>	35	15:34141057-34141063	+	mmu-miR-128-3p	6mer
<i>Mtdh</i>	14	15:34141858-34141864	+	mmu-miR-128-3p	6mer
<i>Rims2</i>	16	15:39684082-39684088	+	mmu-miR-128-3p	6mer
<i>Enpp2</i>	89	15:54839192-54839198	-	mmu-miR-128-3p	6mer
<i>Ago2</i>	37	15:73105587-73105593	-	mmu-miR-128-3p	6mer
<i>Nrbp2</i>	49	15:76085680-76085686	-	mmu-miR-128-3p	6mer
<i>1110038F14Rik</i>	14	15:76950621-76950627	+	mmu-miR-128-3p	6mer
<i>Elfn2</i>	18	15:78671585-78671591	-	mmu-miR-128-3p	6mer
<i>Cbx7</i>	13	15:79918291-79918297	-	mmu-miR-128-3p	6mer
<i>Pdgfb</i>	15	15:79996988-79996994	-	mmu-miR-128-3p	6mer
<i>Syngr1</i>	35	15:80117735-80117741	+	mmu-miR-128-3p	6mer
<i>Cacna1i</i>	98	15:80397731-80397737	+	mmu-miR-128-3p	6mer
<i>Tnrc6b</i>	13	15:80933053-80933059	+	mmu-miR-128-3p	6mer
<i>Tnrc6b</i>	17	15:80936762-80936768	+	mmu-miR-128-3p	6mer
<i>Rbx1</i>	36	15:81475673-81475679	+	mmu-miR-128-3p	6mer
<i>Rangap1</i>	38	15:81705036-81705042	-	mmu-miR-128-3p	6mer
<i>Xrcc6</i>	43	15:82040086-82040092	+	mmu-miR-128-3p	6mer
<i>Srebf2</i>	14	15:82205237-82205243	+	mmu-miR-128-3p	6mer
<i>Tcf20</i>	33	15:82808803-82808809	-	mmu-miR-128-3p	6mer
<i>Scube1</i>	28	15:83606829-83606835	-	mmu-miR-128-3p	6mer
<i>Scube1</i>	28	15:83606960-83606966	-	mmu-miR-128-3p	6mer
<i>Mpped1</i>	27	15:83858083-83858089	+	mmu-miR-128-3p	6mer
<i>Phf21b</i>	43	15:84786321-84786327	-	mmu-miR-128-3p	6mer
<i>Gramd4</i>	36	15:86135542-86135548	+	mmu-miR-128-3p	6mer
<i>Kif21a</i>	207	15:90933623-90933629	-	mmu-miR-128-3p	6mer
<i>Gxylt1</i>	14	15:93244071-93244077	-	mmu-miR-128-3p	6mer
<i>Adcy6</i>	13	15:98591945-98591951	-	mmu-miR-128-3p	6mer
<i>Adcy6</i>	20	15:98592195-98592201	-	mmu-miR-128-3p	6mer
<i>Cacnb3</i>	16	15:98643709-98643715	+	mmu-miR-128-3p	6mer
<i>Arf3</i>	40	15:98737656-98737662	-	mmu-miR-128-3p	6mer
<i>Asic1</i>	38	15:99700242-99700248	+	mmu-miR-128-3p	6mer
<i>Pou6f1</i>	24	15:100577926-100577932	-	mmu-miR-128-3p	6mer
<i>Nudt16l1</i>	66	16:4940906-4940912	+	mmu-miR-128-3p	6mer
<i>Mkl2</i>	27	16:13417336-13417342	+	mmu-miR-128-3p	6mer
<i>Pdxdc1</i>	16	16:13834103-13834109	-	mmu-miR-128-3p	6mer

<i>Abcf3</i>	12	16:20560533-20560539	+	mmu-miR-128-3p	6mer
<i>Ece2</i>	90	16:20645261-20645267	+	mmu-miR-128-3p	6mer
<i>1700021K19Rik</i>	370	16:32823550-32823556	-	mmu-miR-128-3p	6mer
<i>Heg1</i>	39	16:33767993-33767999	+	mmu-miR-128-3p	6mer
<i>Kalrn</i>	109	16:33970397-33970403	-	mmu-miR-128-3p	6mer
<i>Zbtb20</i>	74	16:43619362-43619368	+	mmu-miR-128-3p	6mer
<i>Cd47</i>	14	16:49911822-49911828	+	mmu-miR-128-3p	6mer
<i>Rcan1</i>	44	16:92393390-92393396	-	mmu-miR-128-3p	6mer
<i>Wrb</i>	24	16:96157853-96157859	+	mmu-miR-128-3p	6mer
<i>B3galt5</i>	14	16:96319024-96319030	+	mmu-miR-128-3p	6mer
<i>Pisd-ps2</i>	25	17:3079570-3079576	-	mmu-miR-128-3p	6mer
<i>Mas1</i>	23	17:12841248-12841254	-	mmu-miR-128-3p	6mer
<i>Mrps34</i>	27	17:24896134-24896140	+	mmu-miR-128-3p	6mer
<i>Cramp1l</i>	52	17:24962771-24962777	-	mmu-miR-128-3p	6mer
<i>Pigg</i>	22	17:25926606-25926612	-	mmu-miR-128-3p	6mer
<i>Slc29a1</i>	41	17:45585550-45585556	-	mmu-miR-128-3p	6mer
<i>Gtpbp2</i>	91	17:46168753-46168759	+	mmu-miR-128-3p	6mer
<i>Gtpbp2</i>	91	17:46168828-46168834	+	mmu-miR-128-3p	6mer
<i>Gltscr1l</i>	30	17:46799374-46799380	-	mmu-miR-128-3p	6mer
<i>Taf8</i>	29	17:47489664-47489670	-	mmu-miR-128-3p	6mer
<i>Nfyα</i>	11	17:48388635-48388641	-	mmu-miR-128-3p	6mer
<i>Pja2</i>	13	17:64281888-64281894	-	mmu-miR-128-3p	6mer
<i>Ankrd12</i>	13	17:65970093-65970099	-	mmu-miR-128-3p	6mer
<i>Ehd3</i>	10	17:73831596-73831602	+	mmu-miR-128-3p	6mer
<i>Sos1</i>	19	17:80396684-80396690	-	mmu-miR-128-3p	6mer
<i>Srbd1</i>	18	17:85984593-85984599	-	mmu-miR-128-3p	6mer
<i>Mcfd2</i>	57	17:87255768-87255774	-	mmu-miR-128-3p	6mer
<i>Crem</i>	17	18:3267979-3267985	-	mmu-miR-128-3p	6mer
<i>Kif5b</i>	52	18:6203437-6203443	-	mmu-miR-128-3p	6mer
<i>Aqp4</i>	16	18:15391942-15391948	-	mmu-miR-128-3p	6mer
<i>Iws1</i>	27	18:32103678-32103684	+	mmu-miR-128-3p	6mer
<i>Dnajc18</i>	31	18:35673686-35673692	-	mmu-miR-128-3p	6mer
<i>Pcdh1</i>	42	18:38196793-38196799	-	mmu-miR-128-3p	6mer
<i>Mcc</i>	31	18:44425576-44425582	-	mmu-miR-128-3p	6mer
<i>C330018D20Rik</i>	29	18:56957285-56957291	-	mmu-miR-128-3p	6mer
<i>Ndst1</i>	41	18:60687411-60687417	-	mmu-miR-128-3p	6mer
<i>St8sia3</i>	13	18:64273561-64273567	+	mmu-miR-128-3p	6mer
<i>St8sia3</i>	29	18:64275833-64275839	+	mmu-miR-128-3p	6mer
<i>Onecut2</i>	15	18:64396218-64396224	+	mmu-miR-128-3p	6mer
<i>Gnal</i>	56	18:67223603-67223609	+	mmu-miR-128-3p	6mer
<i>Rnf165</i>	14	18:77458300-77458306	-	mmu-miR-128-3p	6mer
<i>Pitpnm1</i>	15	19:4113800-4113806	+	mmu-miR-128-3p	6mer
<i>Pla2g16</i>	17	19:7587278-7587284	+	mmu-miR-128-3p	6mer
<i>Hnrnpul2</i>	37	19:8833251-8833257	+	mmu-miR-128-3p	6mer
<i>Hnrnpul2</i>	11	19:8834031-8834037	+	mmu-miR-128-3p	6mer
<i>Vldlr</i>	11	19:27252770-27252776	+	mmu-miR-128-3p	6mer
<i>Frat2</i>	27	19:41847015-41847021	-	mmu-miR-128-3p	6mer
<i>Actr1a</i>	28	19:46377692-46377698	-	mmu-miR-128-3p	6mer
<i>Nt5c2</i>	27	19:46888217-46888223	-	mmu-miR-128-3p	6mer
<i>Sorcs1</i>	17	19:50148055-50148061	-	mmu-miR-128-3p	6mer
<i>Add3</i>	23	19:53245366-53245372	+	mmu-miR-128-3p	6mer
<i>Adra2a</i>	34	19:54048853-54048859	+	mmu-miR-128-3p	6mer
<i>Vti1a</i>	33	19:55626074-55626080	+	mmu-miR-128-3p	6mer
<i>Ablim1</i>	10	19:57036808-57036814	-	mmu-miR-128-3p	6mer
<i>Ndor1</i>	13	2:25246344-25246350	-	mmu-miR-128-3p	6mer
<i>Fbxw5</i>	10	2:25505407-25505413	+	mmu-miR-128-3p	6mer
<i>Camsap1</i>	14	2:25928407-25928413	-	mmu-miR-128-3p	6mer
<i>Sdccag3</i>	31	2:26383122-26383128	-	mmu-miR-128-3p	6mer
<i>Wdr5</i>	36	2:27534835-27534841	+	mmu-miR-128-3p	6mer
<i>Olfm1</i>	43	2:28214507-28214513	+	mmu-miR-128-3p	6mer
<i>Gtf3c4</i>	26	2:28825616-28825622	-	mmu-miR-128-3p	6mer
<i>Rapgef1</i>	40	2:29739448-29739454	+	mmu-miR-128-3p	6mer
<i>Urm1</i>	20	2:29844487-29844493	+	mmu-miR-128-3p	6mer
<i>Prrc2b</i>	24	2:32230978-32230984	+	mmu-miR-128-3p	6mer
<i>Stxbp1</i>	50	2:32788393-32788399	-	mmu-miR-128-3p	6mer
<i>Dab2ip</i>	26	2:35728244-35728250	+	mmu-miR-128-3p	6mer

<i>Lhx6</i>	15	2:36082600-36082606	-	mmu-miR-128-3p	6mer
<i>Nr6a1</i>	72	2:38727732-38727738	-	mmu-miR-128-3p	6mer
<i>Fmn1</i>	15	2:53132563-53132569	+	mmu-miR-128-3p	6mer
<i>Scn2a1</i>	29	2:65766622-65766628	+	mmu-miR-128-3p	6mer
<i>Csrnp3</i>	15	2:66023179-66023185	+	mmu-miR-128-3p	6mer
<i>Csrnp3</i>	15	2:66023295-66023301	+	mmu-miR-128-3p	6mer
<i>Gad1</i>	12	2:70601385-70601391	+	mmu-miR-128-3p	6mer
<i>Rapgef4</i>	14	2:72256451-72256457	+	mmu-miR-128-3p	6mer
<i>Rapgef4</i>	24	2:72256713-72256719	+	mmu-miR-128-3p	6mer
<i>Zdhhc5</i>	22	2:84688464-84688470	-	mmu-miR-128-3p	6mer
<i>Ypel4</i>	28	2:84738039-84738045	+	mmu-miR-128-3p	6mer
<i>Trim44</i>	10	2:102304294-102304300	-	mmu-miR-128-3p	6mer
<i>Slc1a2</i>	25	2:102784054-102784060	+	mmu-miR-128-3p	6mer
<i>Slc1a2</i>	15	2:102789014-102789020	+	mmu-miR-128-3p	6mer
<i>Caprin1</i>	17	2:103766147-103766153	-	mmu-miR-128-3p	6mer
<i>Fbxo3</i>	55	2:104060467-104060473	+	mmu-miR-128-3p	6mer
<i>Fmn1</i>	45	2:113710699-113710705	+	mmu-miR-128-3p	6mer
<i>Gpr176</i>	23	2:118276318-118276324	-	mmu-miR-128-3p	6mer
<i>Ankrd63</i>	456	2:118700855-118700861	-	mmu-miR-128-3p	6mer
<i>Ehd4</i>	24	2:120090723-120090729	-	mmu-miR-128-3p	6mer
<i>Shf</i>	17	2:122349163-122349169	-	mmu-miR-128-3p	6mer
<i>Ap4e1</i>	14	2:127066861-127066867	+	mmu-miR-128-3p	6mer
<i>Sirpa</i>	10	2:129630845-129630851	+	mmu-miR-128-3p	6mer
<i>Cds2</i>	14	2:132306510-132306516	+	mmu-miR-128-3p	6mer
<i>Cds2</i>	26	2:132308019-132308025	+	mmu-miR-128-3p	6mer
<i>Plcb1</i>	33	2:135474732-135474738	+	mmu-miR-128-3p	6mer
<i>Btbd3</i>	24	2:138286805-138286811	+	mmu-miR-128-3p	6mer
<i>Kif3b</i>	21	2:153330544-153330550	+	mmu-miR-128-3p	6mer
<i>Ncoa6</i>	29	2:155390842-155390848	-	mmu-miR-128-3p	6mer
<i>Epb4.1I1</i>	23	2:156540811-156540817	+	mmu-miR-128-3p	6mer
<i>Epb4.1I1</i>	16	2:156540973-156540979	+	mmu-miR-128-3p	6mer
<i>Dlgap4</i>	47	2:156764120-156764126	+	mmu-miR-128-3p	6mer
<i>Nnat</i>	17	2:157562066-157562072	+	mmu-miR-128-3p	6mer
<i>Snhg11</i>	11	2:158384495-158384501	+	mmu-miR-128-3p	6mer
<i>Ralgapb</i>	29	2:158497961-158497967	+	mmu-miR-128-3p	6mer
<i>Stk4</i>	46	2:164152287-164152293	+	mmu-miR-128-3p	6mer
<i>Cdh22</i>	16	2:165111839-165111845	-	mmu-miR-128-3p	6mer
<i>Slc35c2</i>	32	2:165276845-165276851	-	mmu-miR-128-3p	6mer
<i>Kcnb1</i>	141	2:167101098-167101104	-	mmu-miR-128-3p	6mer
<i>Kcnb1</i>	56	2:167101550-167101556	-	mmu-miR-128-3p	6mer
<i>Kcnb1</i>	30	2:167103624-167103630	-	mmu-miR-128-3p	6mer
<i>Zfp64</i>	19	2:168925180-168925186	-	mmu-miR-128-3p	6mer
<i>Zfp64</i>	19	2:168925211-168925217	-	mmu-miR-128-3p	6mer
<i>Zfp64</i>	19	2:168925245-168925251	-	mmu-miR-128-3p	6mer
<i>Zfp64</i>	19	2:168925276-168925282	-	mmu-miR-128-3p	6mer
<i>Pmepa1</i>	24	2:173225698-173225704	-	mmu-miR-128-3p	6mer
<i>Stx16</i>	13	2:174097047-174097053	+	mmu-miR-128-3p	6mer
<i>Gm14325</i>	19	2:177830368-177830374	-	mmu-miR-128-3p	6mer
<i>Ppp1r3d</i>	63	2:178412050-178412056	-	mmu-miR-128-3p	6mer
<i>Znf512b</i>	36	2:181583123-181583129	-	mmu-miR-128-3p	6mer
<i>Oprl1</i>	11	2:181720143-181720149	+	mmu-miR-128-3p	6mer
<i>Zfp704</i>	111	3:9432294-9432300	-	mmu-miR-128-3p	6mer
<i>Zfp704</i>	18	3:9432857-9432863	-	mmu-miR-128-3p	6mer
<i>Zmat3</i>	61	3:32337794-32337800	-	mmu-miR-128-3p	6mer
<i>Mccc1</i>	10	3:35959994-35960000	-	mmu-miR-128-3p	6mer
<i>Setd7</i>	14	3:51515480-51515486	-	mmu-miR-128-3p	6mer
<i>Tsc22d2</i>	36	3:58461340-58461346	+	mmu-miR-128-3p	6mer
<i>Mbnl1</i>	30	3:60626953-60626959	+	mmu-miR-128-3p	6mer
<i>Kpna4</i>	13	3:69073561-69073567	-	mmu-miR-128-3p	6mer
<i>Slitrk3</i>	104	3:73048192-73048198	-	mmu-miR-128-3p	6mer
<i>Gria2</i>	12	3:80688005-80688011	-	mmu-miR-128-3p	6mer
<i>Trim2</i>	20	3:84161061-84161067	-	mmu-miR-128-3p	6mer
<i>Syt11</i>	31	3:88744813-88744819	-	mmu-miR-128-3p	6mer
<i>Efna3</i>	12	3:89314938-89314944	-	mmu-miR-128-3p	6mer
<i>Kcnn3</i>	17	3:89669020-89669026	+	mmu-miR-128-3p	6mer
<i>Chrb2</i>	22	3:89753530-89753536	-	mmu-miR-128-3p	6mer

<i>Chtop</i>	10	3:90498576-90498582	-	mmu-miR-128-3p	6mer
<i>Sv2a</i>	25	3:96194506-96194512	+	mmu-miR-128-3p	6mer
<i>Pde4dip</i>	15	3:97690550-97690556	-	mmu-miR-128-3p	6mer
<i>Zfp697</i>	20	3:98428940-98428946	+	mmu-miR-128-3p	6mer
<i>Man1a2</i>	27	3:100563121-100563127	-	mmu-miR-128-3p	6mer
<i>Tspan2</i>	25	3:102769367-102769373	+	mmu-miR-128-3p	6mer
<i>Bcas2</i>	24	3:103178532-103178538	+	mmu-miR-128-3p	6mer
<i>Hipk1</i>	61	3:103743263-103743269	-	mmu-miR-128-3p	6mer
<i>Cyb561d1</i>	31	3:108198562-108198568	-	mmu-miR-128-3p	6mer
<i>Sort1</i>	104	3:108357504-108357510	+	mmu-miR-128-3p	6mer
<i>Gpr88</i>	21	3:116251091-116251097	-	mmu-miR-128-3p	6mer
<i>Agl</i>	38	3:116743181-116743187	-	mmu-miR-128-3p	6mer
<i>D3Bwg0562e</i>	61	3:117320692-117320698	-	mmu-miR-128-3p	6mer
<i>F3</i>	19	3:121734306-121734312	+	mmu-miR-128-3p	6mer
<i>Ank2</i>	25	3:126922022-126922028	-	mmu-miR-128-3p	6mer
<i>Col25a1</i>	54	3:130596124-130596130	+	mmu-miR-128-3p	6mer
<i>H2afz</i>	22	3:137866644-137866650	+	mmu-miR-128-3p	6mer
<i>Rap1gds1</i>	44	3:138926036-138926042	-	mmu-miR-128-3p	6mer
<i>Hs2st1</i>	34	3:144434443-144434449	-	mmu-miR-128-3p	6mer
<i>Necab1</i>	24	4:14953602-14953608	-	mmu-miR-128-3p	6mer
<i>Faxc</i>	15	4:21994470-21994476	+	mmu-miR-128-3p	6mer
<i>Aptx</i>	10	4:40686050-40686056	-	mmu-miR-128-3p	6mer
<i>N28178</i>	17	4:42941864-42941870	+	mmu-miR-128-3p	6mer
<i>Fam214b</i>	12	4:43036432-43036438	-	mmu-miR-128-3p	6mer
<i>Gba2</i>	13	4:43567173-43567179	-	mmu-miR-128-3p	6mer
<i>Rnf38</i>	12	4:44129394-44129400	-	mmu-miR-128-3p	6mer
<i>Fbxo10</i>	10	4:45035500-45035506	-	mmu-miR-128-3p	6mer
<i>Gabbr2</i>	29	4:46664137-46664143	-	mmu-miR-128-3p	6mer
<i>Rad23b</i>	80	4:55390826-55390832	+	mmu-miR-128-3p	6mer
<i>Lpar1</i>	26	4:58436420-58436426	-	mmu-miR-128-3p	6mer
<i>Nfib</i>	31	4:82290713-82290719	-	mmu-miR-128-3p	6mer
<i>Ttc39b</i>	78	4:83222308-83222314	-	mmu-miR-128-3p	6mer
<i>Dab1</i>	34	4:104741907-104741913	+	mmu-miR-128-3p	6mer
<i>Dhcr24</i>	20	4:106588242-106588248	+	mmu-miR-128-3p	6mer
<i>Hectd3</i>	13	4:117003542-117003548	+	mmu-miR-128-3p	6mer
<i>Atp6v0b</i>	18	4:117884412-117884418	-	mmu-miR-128-3p	6mer
<i>AU022252</i>	23	4:119226146-119226152	-	mmu-miR-128-3p	6mer
<i>1110065P20Rik</i>	18	4:124849676-124849682	-	mmu-miR-128-3p	6mer
<i>Grik3</i>	12	4:125712693-125712699	+	mmu-miR-128-3p	6mer
<i>Grik3</i>	14	4:125714015-125714021	+	mmu-miR-128-3p	6mer
<i>Ago1</i>	14	4:126438188-126438194	-	mmu-miR-128-3p	6mer
<i>Phc2</i>	29	4:128752241-128752247	+	mmu-miR-128-3p	6mer
<i>Phc2</i>	29	4:128752253-128752259	+	mmu-miR-128-3p	6mer
<i>Eya3</i>	31	4:132723938-132723944	+	mmu-miR-128-3p	6mer
<i>Sfn</i>	13	4:133600690-133600696	-	mmu-miR-128-3p	6mer
<i>Fbxo42</i>	13	4:141202809-141202815	+	mmu-miR-128-3p	6mer
<i>Kif1b</i>	50	4:149176390-149176396	-	mmu-miR-128-3p	6mer
<i>Per3</i>	14	4:151005276-151005282	-	mmu-miR-128-3p	6mer
<i>Gpr153</i>	53	4:152284885-152284891	+	mmu-miR-128-3p	6mer
<i>Lrrc47</i>	57	4:154020439-154020445	+	mmu-miR-128-3p	6mer
<i>Ski</i>	43	4:155155860-155155866	-	mmu-miR-128-3p	6mer
<i>Gnb1</i>	45	4:155559043-155559049	+	mmu-miR-128-3p	6mer
<i>Gnb1</i>	45	4:155559054-155559060	+	mmu-miR-128-3p	6mer
<i>Cacna2d1</i>	21	5:16371738-16371744	+	mmu-miR-128-3p	6mer
<i>Gnai1</i>	38	5:18265175-18265181	-	mmu-miR-128-3p	6mer
<i>Chpf2</i>	16	5:24592943-24592949	+	mmu-miR-128-3p	6mer
<i>Pisd</i>	79	5:32736551-32736557	-	mmu-miR-128-3p	6mer
<i>Whsc1</i>	15	5:33876835-33876841	+	mmu-miR-128-3p	6mer
<i>Nat8l</i>	55	5:34004730-34004736	+	mmu-miR-128-3p	6mer
<i>Cpeb2</i>	10	5:43288690-43288696	+	mmu-miR-128-3p	6mer
<i>Lcorl</i>	18	5:45733424-45733430	-	mmu-miR-128-3p	6mer
<i>Stim2</i>	24	5:54119669-54119675	+	mmu-miR-128-3p	6mer
<i>Rfc1</i>	14	5:65262129-65262135	-	mmu-miR-128-3p	6mer
<i>Dcun1d4</i>	33	5:73559944-73559950	+	mmu-miR-128-3p	6mer
<i>Sgcb</i>	14	5:73633940-73633946	-	mmu-miR-128-3p	6mer
<i>Usp46</i>	14	5:74001412-74001418	-	mmu-miR-128-3p	6mer

<i>Clock</i>	385	5:76213895-76213901	-	mmu-miR-128-3p	6mer
<i>Mob1b</i>	65	5:88756531-88756537	+	mmu-miR-128-3p	6mer
<i>Dck</i>	16	5:88781933-88781939	+	mmu-miR-128-3p	6mer
<i>Slc4a4</i>	102	5:89236708-89236714	+	mmu-miR-128-3p	6mer
<i>Rchy1</i>	18	5:91957660-91957666	-	mmu-miR-128-3p	6mer
<i>Cdkl2</i>	31	5:92007524-92007530	-	mmu-miR-128-3p	6mer
<i>Mapk10</i>	101	5:102910163-102910169	-	mmu-miR-128-3p	6mer
<i>Sparcl1</i>	27	5:104078714-104078720	-	mmu-miR-128-3p	6mer
<i>Evi5</i>	40	5:107746795-107746801	-	mmu-miR-128-3p	6mer
<i>Evi5</i>	40	5:107746843-107746849	-	mmu-miR-128-3p	6mer
<i>Pgam5</i>	10	5:110259728-110259734	-	mmu-miR-128-3p	6mer
<i>Asphd2</i>	26	5:112385683-112385689	-	mmu-miR-128-3p	6mer
<i>Asphd2</i>	26	5:112385704-112385710	-	mmu-miR-128-3p	6mer
<i>Adrbk2</i>	15	5:112911691-112911697	-	mmu-miR-128-3p	6mer
<i>2900026A02Rik</i>	22	5:113089102-113089108	-	mmu-miR-128-3p	6mer
<i>Mmab</i>	23	5:114431446-114431452	-	mmu-miR-128-3p	6mer
<i>Gltp</i>	12	5:114669949-114669955	-	mmu-miR-128-3p	6mer
<i>Dtx1</i>	39	5:120680160-120680166	-	mmu-miR-128-3p	6mer
<i>Ptpn11</i>	34	5:121132038-121132044	-	mmu-miR-128-3p	6mer
<i>Ptpn11</i>	17	5:121132719-121132725	-	mmu-miR-128-3p	6mer
<i>Atp2a2</i>	84	5:122455931-122455937	-	mmu-miR-128-3p	6mer
<i>Vps33a</i>	24	5:123530372-123530378	-	mmu-miR-128-3p	6mer
<i>Bri3bp</i>	36	5:125455915-125455921	+	mmu-miR-128-3p	6mer
<i>Vkorc1I1</i>	16	5:129983601-129983607	+	mmu-miR-128-3p	6mer
<i>Gatsl2</i>	69	5:134139801-134139807	+	mmu-miR-128-3p	6mer
<i>Bcl7b</i>	14	5:135181299-135181305	+	mmu-miR-128-3p	6mer
<i>Zfp12</i>	39	5:143247381-143247387	+	mmu-miR-128-3p	6mer
<i>Daglb</i>	51	5:143503490-143503496	+	mmu-miR-128-3p	6mer
<i>Cyth3</i>	37	5:143709901-143709907	+	mmu-miR-128-3p	6mer
<i>Lmtk2</i>	43	5:144187213-144187219	+	mmu-miR-128-3p	6mer
<i>Polr1d</i>	10	5:147111059-147111065	+	mmu-miR-128-3p	6mer
<i>Tmem106b</i>	53	6:13084255-13084261	+	mmu-miR-128-3p	6mer
<i>Tmem106b</i>	53	6:13084466-13084472	+	mmu-miR-128-3p	6mer
<i>Klhdc10</i>	66	6:30452898-30452904	+	mmu-miR-128-3p	6mer
<i>Klhdc10</i>	11	6:30454213-30454219	+	mmu-miR-128-3p	6mer
<i>Mtpn</i>	11	6:35509115-35509121	-	mmu-miR-128-3p	6mer
<i>Ubn2</i>	12	6:38502835-38502841	+	mmu-miR-128-3p	6mer
<i>Hnrnpa2b1</i>	16	6:51462438-51462444	-	mmu-miR-128-3p	6mer
<i>Ppm1k</i>	23	6:57506776-57506782	-	mmu-miR-128-3p	6mer
<i>Rmnd5a</i>	88	6:71391504-71391510	-	mmu-miR-128-3p	6mer
<i>Rmnd5a</i>	88	6:71391511-71391517	-	mmu-miR-128-3p	6mer
<i>Reep1</i>	13	6:71810050-71810056	+	mmu-miR-128-3p	6mer
<i>Tet3</i>	35	6:83362775-83362781	-	mmu-miR-128-3p	6mer
<i>Rab11fip5</i>	18	6:85336198-85336204	-	mmu-miR-128-3p	6mer
<i>Add2</i>	88	6:86121562-86121568	+	mmu-miR-128-3p	6mer
<i>Add2</i>	46	6:86124309-86124315	+	mmu-miR-128-3p	6mer
<i>Gmcl1</i>	63	6:86692836-86692842	-	mmu-miR-128-3p	6mer
<i>Mgll</i>	37	6:88826664-88826670	+	mmu-miR-128-3p	6mer
<i>Slc6a6</i>	55	6:91756536-91756542	+	mmu-miR-128-3p	6mer
<i>Slc6a6</i>	55	6:91756660-91756666	+	mmu-miR-128-3p	6mer
<i>Kbtbd8</i>	26	6:95127060-95127066	+	mmu-miR-128-3p	6mer
<i>Arl8b</i>	29	6:108823642-108823648	+	mmu-miR-128-3p	6mer
<i>Grm7</i>	56	6:111566735-111566741	+	mmu-miR-128-3p	6mer
<i>Srgap3</i>	10	6:112721547-112721553	-	mmu-miR-128-3p	6mer
<i>Lhfpl4</i>	53	6:113169256-113169262	-	mmu-miR-128-3p	6mer
<i>Brk1</i>	48	6:113616703-113616709	+	mmu-miR-128-3p	6mer
<i>Tatdn2</i>	13	6:113710889-113710895	+	mmu-miR-128-3p	6mer
<i>Atp2b2</i>	92	6:113747542-113747548	-	mmu-miR-128-3p	6mer
<i>Adipor2</i>	16	6:119354374-119354380	-	mmu-miR-128-3p	6mer
<i>Wnk1</i>	24	6:119924439-119924445	-	mmu-miR-128-3p	6mer
<i>Cecr6</i>	24	6:120489111-120489117	-	mmu-miR-128-3p	6mer
<i>Cecr6</i>	102	6:120489992-120489998	-	mmu-miR-128-3p	6mer
<i>Iqsec3</i>	20	6:121372939-121372945	-	mmu-miR-128-3p	6mer
<i>Iqsec3</i>	15	6:121375154-121375160	-	mmu-miR-128-3p	6mer
<i>Clstn3</i>	34	6:124431285-124431291	-	mmu-miR-128-3p	6mer
<i>Ccnd2</i>	35	6:127126445-127126451	-	mmu-miR-128-3p	6mer

<i>Tspan9</i>	49	6:127963872-127963878	-	mmu-miR-128-3p	6mer
<i>Crebl2</i>	18	6:134856988-134856994	+	mmu-miR-128-3p	6mer
<i>Crebl2</i>	37	6:134857513-134857519	+	mmu-miR-128-3p	6mer
<i>Pde3a</i>	15	6:141499419-141499425	+	mmu-miR-128-3p	6mer
<i>Ccdc9</i>	15	7:16274028-16274034	-	mmu-miR-128-3p	6mer
<i>Ap2s1</i>	31	7:16749221-16749227	+	mmu-miR-128-3p	6mer
<i>Zfp180</i>	12	7:24106358-24106364	+	mmu-miR-128-3p	6mer
<i>Grik5</i>	25	7:25010135-25010141	-	mmu-miR-128-3p	6mer
<i>Gm5113</i>	10	7:30179453-30179459	+	mmu-miR-128-3p	6mer
<i>Emc10</i>	40	7:44490661-44490667	-	mmu-miR-128-3p	6mer
<i>Grin2d</i>	20	7:45832234-45832240	-	mmu-miR-128-3p	6mer
<i>Luzp2</i>	10	7:55266273-55266279	+	mmu-miR-128-3p	6mer
<i>C230091D08Rik</i>	10	7:59307750-59307756	-	mmu-miR-128-3p	6mer
<i>Igf1r</i>	20	7:68231831-68231837	+	mmu-miR-128-3p	6mer
<i>Arrdc4</i>	13	7:68738282-68738288	-	mmu-miR-128-3p	6mer
<i>Sv2b</i>	73	7:75117745-75117751	-	mmu-miR-128-3p	6mer
<i>Ap3s2</i>	46	7:79879824-79879830	-	mmu-miR-128-3p	6mer
<i>Crtc3</i>	51	7:80588678-80588684	-	mmu-miR-128-3p	6mer
<i>Crtc3</i>	51	7:80588760-80588766	-	mmu-miR-128-3p	6mer
<i>Homer2</i>	42	7:81603823-81603829	-	mmu-miR-128-3p	6mer
<i>Arnt2</i>	16	7:84246408-84246414	-	mmu-miR-128-3p	6mer
<i>Fzd4</i>	17	7:89409428-89409434	+	mmu-miR-128-3p	6mer
<i>Rab30</i>	49	7:92836900-92836906	+	mmu-miR-128-3p	6mer
<i>Fam160a2</i>	27	7:105371414-105371420	-	mmu-miR-128-3p	6mer
<i>Tpp1</i>	11	7:105746460-105746466	-	mmu-miR-128-3p	6mer
<i>Olfml1</i>	20	7:107590462-107590468	+	mmu-miR-128-3p	6mer
<i>Tub</i>	46	7:109032957-109032963	+	mmu-miR-128-3p	6mer
<i>Rps15a</i>	27	7:118105285-118105291	-	mmu-miR-128-3p	6mer
<i>Usp31</i>	27	7:121642526-121642532	-	mmu-miR-128-3p	6mer
<i>Usp31</i>	13	7:121648063-121648069	-	mmu-miR-128-3p	6mer
<i>Gga2</i>	18	7:121988770-121988776	-	mmu-miR-128-3p	6mer
<i>Prkcb</i>	27	7:122634169-122634175	+	mmu-miR-128-3p	6mer
<i>Tnrc6a</i>	39	7:123194150-123194156	+	mmu-miR-128-3p	6mer
<i>Ate1</i>	11	7:130391667-130391673	-	mmu-miR-128-3p	6mer
<i>Chst15</i>	31	7:132236856-132236862	-	mmu-miR-128-3p	6mer
<i>Deaf1</i>	88	7:141297448-141297454	-	mmu-miR-128-3p	6mer
<i>Dusp8</i>	33	7:142081700-142081706	-	mmu-miR-128-3p	6mer
<i>Nap1l4</i>	22	7:143513813-143513819	-	mmu-miR-128-3p	6mer
<i>Ctxn1</i>	140	8:4258313-4258319	-	mmu-miR-128-3p	6mer
<i>Elavl1</i>	46	8:4285688-4285694	-	mmu-miR-128-3p	6mer
<i>Arhgef7</i>	11	8:11825421-11825427	+	mmu-miR-128-3p	6mer
<i>Atp11a</i>	28	8:12865966-12865972	+	mmu-miR-128-3p	6mer
<i>Kbtbd11</i>	13	8:15031451-15031457	+	mmu-miR-128-3p	6mer
<i>Vps36</i>	186	8:22218717-22218723	+	mmu-miR-128-3p	6mer
<i>Ank1</i>	108	8:23148598-23148604	+	mmu-miR-128-3p	6mer
<i>Tm2d2</i>	53	8:25023190-25023196	+	mmu-miR-128-3p	6mer
<i>Hgsnat</i>	27	8:25944829-25944835	-	mmu-miR-128-3p	6mer
<i>Erlin2</i>	16	8:27036747-27036753	+	mmu-miR-128-3p	6mer
<i>Tnks</i>	16	8:34829732-34829738	-	mmu-miR-128-3p	6mer
<i>Mfhas1</i>	13	8:35678024-35678030	+	mmu-miR-128-3p	6mer
<i>Psd3</i>	16	8:67689856-67689862	-	mmu-miR-128-3p	6mer
<i>Csgalnact1</i>	27	8:68358255-68358261	-	mmu-miR-128-3p	6mer
<i>Nacc1</i>	44	8:84671751-84671757	-	mmu-miR-128-3p	6mer
<i>N4bp1</i>	11	8:86841258-86841264	-	mmu-miR-128-3p	6mer
<i>N4bp1</i>	11	8:86841265-86841271	-	mmu-miR-128-3p	6mer
<i>Gnao1</i>	15	8:93957682-93957688	+	mmu-miR-128-3p	6mer
<i>Gnao1</i>	11	8:93961446-93961452	+	mmu-miR-128-3p	6mer
<i>D230025D16Rik</i>	36	8:105251712-105251718	+	mmu-miR-128-3p	6mer
<i>Pskh1</i>	12	8:105930523-105930529	+	mmu-miR-128-3p	6mer
<i>Pskh1</i>	63	8:105931018-105931024	+	mmu-miR-128-3p	6mer
<i>Sntb2</i>	27	8:107012198-107012204	+	mmu-miR-128-3p	6mer
<i>Sntb2</i>	26	8:107013565-107013571	+	mmu-miR-128-3p	6mer
<i>Atxn11</i>	21	8:109730814-109730820	-	mmu-miR-128-3p	6mer
<i>Il34</i>	34	8:110741929-110741935	-	mmu-miR-128-3p	6mer
<i>Cmip</i>	29	8:117462078-117462084	+	mmu-miR-128-3p	6mer
<i>Emc8</i>	28	8:120656765-120656771	-	mmu-miR-128-3p	6mer

<i>Slc7a5</i>	19	8:121882376-121882382	-	mmu-miR-128-3p	6mer
<i>Cbfa2t3</i>	11	8:122630184-122630190	-	mmu-miR-128-3p	6mer
<i>Ankrd11</i>	26	8:122900551-122900557	-	mmu-miR-128-3p	6mer
<i>Egln1</i>	17	8:124910536-124910542	-	mmu-miR-128-3p	6mer
<i>Gria4</i>	26	9:4420113-4420119	-	mmu-miR-128-3p	6mer
<i>Fat3</i>	13	9:15914284-15914290	-	mmu-miR-128-3p	6mer
<i>Fat3</i>	13	9:15914317-15914323	-	mmu-miR-128-3p	6mer
<i>Tmed1</i>	35	9:21507994-21508000	-	mmu-miR-128-3p	6mer
<i>BC018242</i>	17	9:21947612-21947618	+	mmu-miR-128-3p	6mer
<i>Arhgap32</i>	18	9:32264211-32264217	+	mmu-miR-128-3p	6mer
<i>Ddx6</i>	27	9:44638203-44638209	+	mmu-miR-128-3p	6mer
<i>Scn2b</i>	43	9:45126667-45126673	+	mmu-miR-128-3p	6mer
<i>Scn2b</i>	24	9:45127151-45127157	+	mmu-miR-128-3p	6mer
<i>Scn4b</i>	29	9:45152163-45152169	+	mmu-miR-128-3p	6mer
<i>Pafah1b2</i>	38	9:45968128-45968134	-	mmu-miR-128-3p	6mer
<i>Ptpn9</i>	15	9:57061392-57061398	+	mmu-miR-128-3p	6mer
<i>Cln6</i>	44	9:62851422-62851428	+	mmu-miR-128-3p	6mer
<i>Rab11a</i>	12	9:64715569-64715575	-	mmu-miR-128-3p	6mer
<i>Tmod2</i>	50	9:75571742-75571748	-	mmu-miR-128-3p	6mer
<i>Elovl5</i>	10	9:77983036-77983042	+	mmu-miR-128-3p	6mer
<i>Snap91</i>	13	9:86766060-86766066	-	mmu-miR-128-3p	6mer
<i>Chst2</i>	11	9:95401144-95401150	-	mmu-miR-128-3p	6mer
<i>Slc25a36</i>	15	9:97076329-97076335	-	mmu-miR-128-3p	6mer
<i>Rab6b</i>	34	9:103181666-103181672	+	mmu-miR-128-3p	6mer
<i>Rab6b</i>	22	9:103182814-103182820	+	mmu-miR-128-3p	6mer
<i>Rab6b</i>	17	9:103185207-103185213	+	mmu-miR-128-3p	6mer
<i>Uba5</i>	23	9:104047331-104047337	-	mmu-miR-128-3p	6mer
<i>Mon1a</i>	15	9:107903087-107903093	+	mmu-miR-128-3p	6mer
<i>Map4</i>	23	9:110003840-110003846	+	mmu-miR-128-3p	6mer
<i>Arpp21</i>	47	9:112065802-112065808	-	mmu-miR-128-3p	6mer
<i>Arpp21</i>	29	9:112182543-112182549	-	mmu-miR-128-3p	6mer
<i>Oxsr1</i>	19	9:119304878-119304884	-	mmu-miR-128-3p	6mer
<i>Myrip</i>	49	9:120472882-120472888	+	mmu-miR-128-3p	6mer
<i>Usp9x</i>	10	X:13172279-13172285	+	mmu-miR-128-3p	6mer
<i>Sept6</i>	76	X:36912918-36912924	-	mmu-miR-128-3p	6mer
<i>Fgf13</i>	11	X:59063089-59063095	-	mmu-miR-128-3p	6mer
<i>Slitrk4</i>	40	X:64270344-64270350	-	mmu-miR-128-3p	6mer
<i>Cd99l2</i>	15	X:71420414-71420420	-	mmu-miR-128-3p	6mer
<i>Prrg3</i>	29	X:71967655-71967661	+	mmu-miR-128-3p	6mer
<i>Prrg3</i>	11	X:71968315-71968321	+	mmu-miR-128-3p	6mer
<i>Atp2b3</i>	35	X:73571723-73571729	+	mmu-miR-128-3p	6mer
<i>Mecp2</i>	20	X:74031328-74031334	-	mmu-miR-128-3p	6mer
<i>Rab39b</i>	24	X:75571619-75571625	-	mmu-miR-128-3p	6mer
<i>Pls3</i>	73	X:75786805-75786811	-	mmu-miR-128-3p	6mer
<i>Gpr165</i>	46	X:96719750-96719756	+	mmu-miR-128-3p	6mer
<i>Slc16a2</i>	43	X:103699373-103699379	-	mmu-miR-128-3p	6mer
<i>Drp2</i>	20	X:134456256-134456262	+	mmu-miR-128-3p	6mer
<i>Pak3</i>	40	X:143797716-143797722	+	mmu-miR-128-3p	6mer
<i>Gpm6b</i>	19	X:166388293-166388299	+	mmu-miR-128-3p	6mer
<i>Frmpd4</i>	166	X:167472239-167472245	-	mmu-miR-128-3p	6mer

Table S3. 154 RISC-associated miR-128 target genes that show increased ribosome-association in miR-128 deficient D1-neurons.

D1-neuron TRAP analysis (mRNAs that show increase ribosome association in wild type versus miR-128- deficient D1-neurons)		RISC-associated 3'UTR mRNAs in adult neurons					
Gene Symbol	p-value	Fold Change	# Reads in Cluster	Gene Title	Entrez Gene	Probe Set ID	
9530068E07Rik	3.2E-02	1.36	16	RIKEN cDNA 9530068E07 gene	213673	1427108_at	
Abcb9	1.1E-02	1.42	18	ATP-binding cassette, sub-family B (MDR/TAP), member 9	56325	1416263_at	
Acvr1c	2.6E-02	1.26	108	activin A receptor, type IC	269275	1438309_at	
Acvr1c	2.7E-02	1.44	108	activin A receptor, type IC	269275	1443225_at	
Agl	4.5E-02	1.40	38	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	77559	1431032_at	
Al593442	3.8E-03	1.22	51	expressed sequence Al593442	330941	1434052_at	
Ak2	3.6E-03	1.36	12	adenylate kinase 2	11637	1448450_at	
Ak3	5.8E-03	1.22	10	adenylate kinase 3	56248	1423717_at	
Ankrd40	3.6E-02	1.31	20	ankyrin repeat domain 40	71452	1453744_a_at	
Aplp2	2.5E-02	1.38	114	amyloid beta (A4) precursor-like protein 2	11804	1421889_a_at	
Aplp2	4.5E-02	1.16	114	amyloid beta (A4) precursor-like protein 2	11804	1421888_x_at	
Arfrp1	1.9E-02	1.14	12	ADP-ribosylation factor related protein 1	76688	1425507_at	
Arfrp1	2.2E-02	1.24	12	ADP-ribosylation factor related protein 1	76688	1425508_s_at	
Arpp21	1.0E-04	1.31	47	cyclic AMP-regulated phosphoprotein, 21	74100	1419028_at	
Arrdc4	3.0E-03	1.40	13	arrestin domain containing 4	66412	1426818_at	
Atp2a2	1.2E-02	1.16	84	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	11938	1452363_a_at	
AU022252	2.2E-02	1.24	23	expressed sequence AU022252	230696	1438226_at	
B3galt1	3.9E-02	1.63	10	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	26877	1460509_at	
BC030336	4.2E-02	1.38	44	cDNA sequence BC030336	233812	1434075_at	
Bmi1	2.0E-02	1.25	23	Bmi1 polycomb ring finger oncogene	12151	1448733_at	
Bmi1	3.4E-02	1.27	23	Bmi1 polycomb ring finger oncogene	12151	1417493_at	
Bri3bp	2.9E-02	1.29	45	Bri3 binding protein	76809	1438198_at	
Cacna2d3	6.4E-03	1.26	11	calcium channel, voltage-dependent, alpha2/delta subunit 3	12294	1419225_at	
Cacng2	2.1E-02	1.22	19	calcium channel, voltage-dependent, gamma subunit 2	12300	1440210_at	
Cacul1	1.9E-02	1.58	10	RIKEN cDNA 2700078E11 gene	78832	1424982_a_at	
Car7	2.6E-02	1.32	39	carbonic anhydrase 7	12354	1443824_s_at	
Casd1	3.4E-02	1.09	13	CAS1 domain containing 1	213819	1451980_at	
Ccdc47	4.0E-02	1.21	42	coiled-coil domain containing 47	67163	1424636_at	
Cndp2	4.3E-05	1.46	10	CNDP dipeptidase 2 (metallopeptidase M20 family)	66054	1460177_at	
Cndp2	1.8E-02	1.20	10	CNDP dipeptidase 2 (metallopeptidase M20 family)	66054	1448263_a_at	
Cnot7	3.5E-02	1.38	12	CCR4-NOT transcription complex, subunit 7	18983	1460665_a_at	

<i>Crem</i>	5.1E-03	1.26	17	cAMP responsive element modulator	12916	1418322_at
<i>Csnk1d</i>	4.1E-02	1.61	12	casein kinase 1, delta	104318	1449932_at
<i>Cwc25</i>	3.6E-02	1.20	20	CWC25 spliceosome-associated protein homolog (S. cerevisiae)	67480	1428759_s_at
<i>D3Bwg0562e</i>	4.5E-02	1.25	61	DNA segment, Chr 3, Brigham & Women's Genetics 0562 expressed	229791	1434685_at
<i>Dcaf5</i>	3.8E-02	1.41	10	DDB1 and CUL4 associated factor 5	320808	1455354_at
<i>Dnajc27</i>	2.0E-02	1.35	19	DnAJ (Hsp40) homolog, subfamily C, member 27	217378	1435117_a_at
<i>Egln1</i>	2.4E-02	1.20	17	EGL nine homolog 1 (C. elegans)	112405	1423785_at
<i>Elfn2</i>	1.4E-02	1.29	18	leucine rich repeat and fibronectin type III, extracellular 2	207393	1456202_at
<i>Fads1</i>	2.2E-03	1.33	248	fatty acid desaturase 1	76267	1423680_at
<i>Fam102a</i>	6.3E-03	1.30	17	family with sequence similarity 102, member A	98952	1426893_at
<i>Fam126b</i>	2.7E-02	1.28	81	family with sequence similarity 126, member B	213056	1456320_at
<i>Fam168b</i>	4.7E-02	1.09	89	family with sequence similarity 168, member B	214469	1434018_at
<i>Fam171a1</i>	1.3E-02	1.33	12	family with sequence similarity 171, member A1	269233	1438402_at
<i>Flrt3</i>	2.6E-02	1.13	44	fibronectin leucine rich transmembrane protein 3	71436	1429310_at
<i>Flrt3</i>	4.2E-02	1.22	44	fibronectin leucine rich transmembrane protein 3	71436	1453102_at
<i>Frrs1l</i>	2.6E-02	1.39	10	RIKEN cDNA 6430704M03 gene	230235	1437640_at
<i>Fxr2</i>	1.8E-02	1.18	45	fragile X mental retardation, autosomal homolog 2	23879	1422522_at
<i>Gad1</i>	3.0E-02	1.78	12	glutamic acid decarboxylase 1	14415	1416562_at
<i>Gad1</i>	3.2E-02	1.11	12	glutamic acid decarboxylase 1	14415	1416561_at
<i>Gas7</i>	2.3E-02	1.30	92	growth arrest specific 7	14457	1417859_at
<i>Gpm6b</i>	1.4E-02	1.12	19	glycoprotein m6b	14758	1423091_a_at
<i>Gpm6b</i>	3.6E-02	1.37	19	glycoprotein m6b	14758	1425942_a_at
<i>Gpr176</i>	4.7E-02	1.18	23	G protein-coupled receptor 176	381413	1442116_at
<i>Gpr88</i>	2.8E-02	1.17	21	G-protein coupled receptor 88	64378	1423171_at
<i>Gps1</i>	3.4E-02	1.22	10	G protein pathway suppressor 1	209318	1415699_a_at
<i>Gsg1l</i>	6.8E-03	1.36	38	GSG1-like	269994	1436013_at
<i>H3f3b</i>	2.5E-04	1.34	14	H3 histone, family 3B	15081	1420376_a_at
<i>Hgsnat</i>	2.1E-02	1.18	27	heparan-alpha-glucosaminide N-acetyltransferase	52120	1436580_at
<i>Hs2st1</i>	4.5E-02	1.24	34	heparan sulfate 2-O-sulfotransferase 1	23908	1450729_at
<i>Iffo2</i>	9.9E-03	1.18	21	intermediate filament family orphan 2	212632	1435455_at
<i>Il34</i>	4.5E-02	1.40	34	interleukin 34	76527	1431920_a_at
<i>Insm1</i>	1.4E-03	1.34	35	insulinoma-associated 1	53626	1421399_at
<i>Insm1</i>	2.9E-02	1.32	35	insulinoma-associated 1	53626	1455865_at
<i>Kbtbd8</i>	1.3E-02	1.24	26	kelch repeat and BTB (POZ) domain containing 8	243574	1433902_at
<i>Kcnma1</i>	3.7E-02	1.20	15	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	16531	1428948_at
<i>Kcnma1</i>	4.3E-02	1.16	15	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	16531	1425987_a_at
<i>Kctd3</i>	2.9E-02	1.32	26	potassium channel tetramerisation domain containing 3	226823	1436811_at
<i>Kif1a</i>	1.4E-02	1.40	16	kinesin family member 1A	16560	1450108_at
<i>Lhfpl2</i>	4.9E-02	1.15	11	lipoma HMGIC fusion partner-like 2	218454	1434129_s_at
<i>Lhfpl4</i>	3.6E-02	1.21	53	lipoma HMGIC fusion partner-like protein 4	269788	1436553_at
<i>Lmbr1</i>	3.0E-02	2.29	13	limb region 1	56873	1425605_a_at
<i>Lpgat1</i>	7.6E-03	1.31	85	lysophosphatidylglycerol acyltransferase 1	226856	1435327_at

<i>Man1a2</i>	1.1E-02	1.21	27	mannosidase, alpha, class 1A, member 2	17156	1434395_at
<i>Man1a2</i>	3.3E-02	1.19	27	mannosidase, alpha, class 1A, member 2	17156	1420977_at
<i>Mapk14</i>	3.3E-02	1.11	21	mitogen-activated protein kinase 14	26416	1416703_at
<i>Meaf6</i>	7.1E-04	1.44	15	MYST/Esa1-associated factor 6	70088	1457977_at
<i>Msl1</i>	3.6E-02	1.25	17	male-specific lethal 1 homolog (Drosophila)	74026	1428872_at
<i>Mtch1</i>	1.9E-02	1.19	31	mitochondrial carrier homolog 1 (<i>C. elegans</i>)	56462	1460718_s_at
<i>Mtx3</i>	5.2E-03	1.61	22	metaxin 3	382793	1434806_at
<i>Mtx3</i>	4.6E-02	1.15	22	metaxin 3	382793	1434807_s_at
<i>Ndst1</i>	4.4E-02	1.30	41	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	15531	1428367_at
<i>Ndufab1</i>	1.4E-02	1.28	27	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	70316	1458678_at
<i>Neto1</i>	4.7E-03	1.17	26	neuropilin (NRP) and tolloid (TLL)-like 1	246317	1456283_at
<i>Neto2</i>	1.9E-03	1.34	20	neuropilin (NRP) and tolloid (TLL)-like 2	74513	1436309_at
<i>Nup50</i>	4.5E-03	1.30	23	nucleoporin 50	18141	1428328_at
<i>Obfc2a</i>	2.2E-02	1.13	12	oligonucleotide/oligosaccharide-binding fold containing 2A	109019	1426806_at
<i>Oprl1</i>	2.5E-02	1.16	11	opioid receptor-like 1	18389	1426204_a_at
<i>Ormdl3</i>	1.1E-02	1.50	15	ORM1-like 3 (<i>S. cerevisiae</i>)	66612	1419450_at
<i>Paip2</i>	1.3E-02	1.14	37	polyadenylate-binding protein-interacting protein 2	67869	1448493_at
<i>Pard6b</i>	8.4E-03	1.38	17	par-6 (partitioning defective 6) homolog beta (<i>C. elegans</i>)	58220	1423174_a_at
<i>Pde10a</i>	3.4E-02	1.11	73	phosphodiesterase 10A	23984	1439618_at
<i>Pde10a</i>	3.9E-02	1.57	73	phosphodiesterase 10A	23984	1458499_at
<i>Pdgfb</i>	2.7E-02	1.20	15	platelet derived growth factor, B polypeptide	18591	1450414_at
<i>Pea15a</i>	9.9E-04	1.63	49	phosphoprotein enriched in astrocytes 15A	18611	1416407_at
<i>Pfdn2</i>	1.4E-02	1.17	17	prefoldin 2	18637	1421950_at
<i>Pigg</i>	1.2E-02	1.26	22	phosphatidylinositol glycan anchor biosynthesis, class Q	14755	1415946_at
<i>Pmepa1</i>	2.2E-03	1.17	24	prostate transmembrane protein, androgen induced 1	65112	1422706_at
<i>Prkx</i>	6.3E-04	1.59	270	protein kinase, X-linked	19108	1424286_at
<i>Prkx</i>	2.0E-02	1.32	270	protein kinase, X-linked	19108	1451299_at
<i>Prr3</i>	2.5E-02	1.19	26	proline-rich polypeptide 3	75210	1424145_at
<i>Ptpn9</i>	2.5E-03	1.38	15	protein tyrosine phosphatase, non-receptor type 9	56294	1451037_at
<i>Pum2</i>	1.5E-02	1.29	47	pumilio 2 (<i>Drosophila</i>)	80913	1418017_at
<i>Pygb</i>	2.4E-02	1.20	34	brain glycogen phosphorylase	110078	1433504_at
<i>Rab14</i>	3.7E-02	1.19	39	RAB14, member RAS oncogene family	68365	1415686_at
<i>Rab39b</i>	9.9E-03	1.31	24	RAB39B, member RAS oncogene family	67790	1435014_at
<i>Rcan2</i>	3.7E-02	1.09	88	regulator of calcineurin 2	53901	1421425_a_at
<i>Rdh11</i>	1.2E-03	1.61	17	retinol dehydrogenase 11	17252	1449209_a_at
<i>Rgs2</i>	7.5E-03	1.18	15	regulator of G-protein signaling 2	19735	1419248_at
<i>Rgs6</i>	3.0E-02	1.11	22	regulator of G-protein signaling 6	50779	1452399_at
<i>Rgs8</i>	5.1E-04	1.19	81	regulator of G-protein signaling 8	67792	1453060_at
<i>Rmnd5a</i>	1.6E-02	1.19	88	required for meiotic nuclear division 5 homolog A (<i>S. cerevisiae</i>)	68477	1426884_at
<i>Rmnd5a</i>	2.7E-02	1.62	88	required for meiotic nuclear division 5 homolog A (<i>S. cerevisiae</i>)	68477	1431068_at
<i>Rnf149</i>	3.7E-03	1.45	16	ring finger protein 149	67702	1429321_at
<i>Rnh1</i>	2.6E-04	1.60	68	ribonuclease/angiogenin inhibitor 1	107702	1451201_s_at

<i>Rpn1</i>	4.7E-02	1.11	29	ribophorin I	103963	1438943_x_at
<i>Rps6</i>	4.7E-02	1.19	116	ribosomal protein S6	20104	1416142_at
<i>Samd10</i>	6.8E-05	1.63	54	sterile alpha motif domain containing 10	229011	1435756_at
<i>Samd8</i>	9.8E-03	1.18	30	sterile alpha motif domain containing 8	67630	1434402_at
<i>Scn2b</i>	1.2E-02	1.17	43	sodium channel, voltage-gated, type II, beta	72821	1436134_at
<i>Scn2b</i>	2.7E-02	1.60	43	sodium channel, voltage-gated, type II, beta	72821	1430648_at
<i>Scn4b</i>	6.8E-03	1.14	29	sodium channel, type IV, beta	399548	1434008_at
<i>Sec61a1</i>	7.7E-04	1.41	84	Sec61 alpha 1 subunit (<i>S. cerevisiae</i>)	53421	1448242_at
<i>Sec61a1</i>	3.9E-02	1.35	84	Sec61 alpha 1 subunit (<i>S. cerevisiae</i>)	53421	1416189_a_at
<i>Sec61a1</i>	4.1E-02	1.24	84	Sec61 alpha 1 subunit (<i>S. cerevisiae</i>)	53421	1434986_a_at
<i>Setd8</i>	1.1E-02	1.21	14	SET domain containing (lysine methyltransferase) 8	67956	1460687_at
<i>Sez6</i>	9.4E-04	1.35	41	seizure related gene 6	20370	1427674_a_at
<i>Sgcb</i>	1.6E-06	1.98	24	sarcoglycan, beta (dystrophin-associated glycoprotein)	24051	1436678_at
<i>Sgcb</i>	2.5E-05	1.77	24	sarcoglycan, beta (dystrophin-associated glycoprotein)	24051	1419668_at
<i>Sgpp1</i>	2.0E-03	1.45	17	sphingosine-1-phosphate phosphatase 1	81535	1420822_s_at
<i>Sgpp1</i>	2.8E-02	1.43	17	sphingosine-1-phosphate phosphatase 1	81535	1420821_at
<i>Sirpa</i>	1.7E-02	1.15	10	signal-regulatory protein alpha	19261	1416985_at
<i>Sirpa</i>	4.8E-02	1.40	10	signal-regulatory protein alpha	19261	1448534_at
<i>Slc1a1</i>	4.6E-02	1.21	16	solute carrier family 1 (high affinity glutamate transporter), member 1	20510	1425415_a_at
<i>Slc35f3</i>	9.1E-04	1.37	39	solute carrier family 35, member F3	210027	1456764_at
<i>Slc37a3</i>	1.8E-02	1.28	25	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	72144	1453915_a_at
<i>Slc39a11</i>	5.0E-06	1.58	328	solute carrier family 39 (metal ion transporter), member 11	69806	1424905_a_at
<i>Slc39a13</i>	4.3E-02	1.13	92	solute carrier family 39 (metal ion transporter), member 13	68427	1423926_at
<i>Slc4a4</i>	5.0E-02	1.23	102	solute carrier family 4 (anion exchanger), member 4	54403	1452071_at
<i>Slc6a1</i>	1.1E-02	1.27	14	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	232333	1452142_at
<i>Sos1</i>	2.7E-02	1.17	19	son of sevenless homolog 1 (<i>Drosophila</i>)	20662	1434389_at
<i>Srsf13b</i>	8.4E-03	1.39	40	serine/arginine-rich splicing factor 13B	272009	1437168_at
<i>Ssr3</i>	1.8E-02	1.28	14	signal sequence receptor, gamma	67437	1415700_a_at
<i>Ssr3</i>	2.1E-02	1.08	14	signal sequence receptor, gamma	67437	1447053_x_at
<i>St8sia3</i>	8.9E-03	1.19	29	ST8 alpha-N-acetyl-neuraminate alpha-2,8-sialyltransferase 3	20451	1440029_at
<i>St8sia3</i>	3.6E-02	1.20	29	ST8 alpha-N-acetyl-neuraminate alpha-2,8-sialyltransferase 3	20451	1451008_at
<i>Stim2</i>	8.8E-03	1.20	24	stromal interaction molecule 2	116873	1434219_at
<i>Stx16</i>	2.9E-02	1.14	13	syntaxin 16	228960	1429237_at
<i>Susd4</i>	3.9E-02	1.11	52	sushi domain containing 4	96935	1460593_at
<i>Svop</i>	6.1E-03	1.25	20	SV2 related protein	68666	1452663_at
<i>Syt11</i>	1.3E-02	1.44	31	synaptotagmin XI	229521	1449264_at
<i>Szrd1/D4Ert22e</i>	3.8E-04	1.68	16	SUZ RNA binding domain containing 1	213491	1434482_at
<i>Szrd1/D4Ert22e</i>	2.3E-03	1.40	16	SUZ RNA binding domain containing 1	213491	1454981_at
<i>Tex2</i>	7.0E-03	1.23	57	testis expressed gene 2	21763	1452213_at
<i>Tex261</i>	1.4E-02	1.42	20	testis expressed gene 261	21766	1452768_at
<i>Tgoln1</i>	2.8E-02	1.18	22	trans-golgi network protein	22134	1423309_at
<i>Tial1</i>	1.4E-02	1.09	23	Tia1 cytotoxic granule-associated RNA binding protein-like 1	21843	1426352_s_at

<i>Tm2d2</i>	1.1E-02	1.24	53	TM2 domain containing 2	69742	1433473_x_at
<i>Tm2d2</i>	3.3E-02	1.22	53	TM2 domain containing 2	69742	1439235_x_at
<i>Tm2d2</i>	3.6E-02	1.31	53	TM2 domain containing 2	69742	1451134_a_at
<i>Tmbim6</i>	2.1E-03	1.16	18	transmembrane BAX inhibitor motif containing 6	110213	1451586_at
<i>Tmem179</i>	1.0E-02	1.35	27	transmembrane protein 179	104885	1436754_at
<i>Tmem206</i>	3.1E-02	1.21	41	transmembrane protein 206	66950	1448552_s_at
<i>Tmem246</i>	1.7E-03	1.22	24	RIKEN cDNA 2810432L12 gene	67063	1423679_at
<i>Tmem64</i>	2.5E-03	1.48	10	transmembrane protein 64	100201	1434307_at
<i>Tmem64</i>	1.5E-02	1.34	10	transmembrane protein 64	100201	1454709_at
<i>Tmem64</i>	2.4E-02	1.30	10	transmembrane protein 64	100201	1433735_a_at
<i>Tmem87b</i>	1.6E-02	1.13	16	transmembrane protein 87B	72477	1429337_at
<i>Trim2</i>	3.3E-02	1.31	20	tripartite motif-containing 2	80890	1448551_a_at
<i>Trove2</i>	1.8E-05	1.69	199	TROVE domain family, member 2	20822	1423433_at
<i>Trove2</i>	4.3E-04	1.37	199	TROVE domain family, member 2	20822	1436533_at
<i>Trove2</i>	1.1E-02	1.39	199	TROVE domain family, member 2	20822	1436535_at
<i>Trove2</i>	1.4E-02	1.40	199	TROVE domain family, member 2	20822	1436534_at
<i>Tlli11</i>	4.1E-02	1.14	15	tubulin tyrosine ligase-like family, member 11	74410	1430064_at
<i>Tub</i>	1.7E-02	1.25	46	tubby candidate gene	22141	1420925_at
<i>Tug1</i>	9.7E-03	1.31	69	taurine upregulated gene 1	544752	1415708_at
<i>Tug1</i>	3.8E-02	1.84	69	Taurine upregulated gene 1	544752	1456398_at
<i>Ube2e2</i>	1.8E-02	1.15	14	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	218793	1424358_at
<i>Ugcg</i>	3.0E-02	1.34	32	UDP-glucose ceramide glucosyltransferase	22234	1435133_at
<i>Usp9x</i>	3.3E-02	1.46	10	ubiquitin specific peptidase 9, X chromosome	22284	1450038_s_at
<i>Usp9x</i>	3.9E-02	1.55	10	ubiquitin specific peptidase 9, X chromosome	22284	1450037_at
<i>Wbp1/D19Wsu162e</i>	6.6E-03	1.62	26	DNA segment, Chr 19, Wayne State University 162, expressed	226178	1433717_at
<i>Wbp1/D19Wsu162e</i>	3.0E-02	1.34	26	DNA segment, Chr 19, Wayne State University 162, expressed	226178	1425529_s_at
<i>Whsc1</i>	2.2E-02	1.19	15	Wolf-Hirschhorn syndrome candidate 1 (human)	107823	1455228_at
<i>Wrb</i>	1.5E-02	1.31	24	tryptophan rich basic protein	71446	1460446_at
<i>Zdhhc21</i>	4.0E-03	1.44	50	zinc finger, DHHC domain containing 21	68268	1435104_at
<i>Zfp652</i>	1.0E-02	1.41	39	zinc finger protein 652	268469	1434720_at
<i>Zfp652</i>	4.7E-02	1.15	39	zinc finger protein 652	268469	1456520_at
<i>Zmat3</i>	1.4E-02	1.12	61	zinc finger matrin type 3	22401	1449353_at

Table S4. miR-128 targets in D1-neurons are enriched in ion channels, ion transporters, and signaling proteins.

Group	Gene Symbol	Gene Title	Entrez Gene	Anti-seizure drug
Ion channels and transporters	<i>Cacna2d3</i> <i>Cacng2</i> <i>Kcnma1</i> <i>Kctd3</i> <i>Kcnma1</i> <i>Kctd3</i> <i>Scn2b</i> <i>Scn4b</i> <i>Slc35f3</i> <i>Slc39a11</i> <i>Slc39a13</i> <i>Slc4a4</i> <i>Stim2</i>	calcium channel, voltage-dependent, alpha2/delta subunit 3 calcium channel, voltage-dependent, gamma subunit 2 potassium large conductance calcium-activated channel, subfamily M, alpha member 1 potassium channel tetramerisation domain containing 3 potassium large conductance calcium-activated channel, subfamily M, alpha member 1 potassium channel tetramerisation domain containing 3 sodium channel, voltage-gated, type II, beta sodium channel, type IV, beta solute carrier family 35, member F3 solute carrier family 39 (metal ion transporter), member 11 solute carrier family 39 (metal ion transporter), member 13 solute carrier family 4 (anion exchanger), member 4 stromal interaction molecule 2	12294 12300 16531 226823 16531 226823 72821 399548 210027 69806 68427 54403 116873	Pregabalin Pregabalin Riluzole Riluzole
Glutamate and GABA signaling	<i>Gad1</i> <i>Gsg1l</i> <i>Slc6a1</i> <i>Slc1a1</i> <i>Neto1</i> <i>Neto2</i>	glutamic acid decarboxylase 1 GSG1-like solute carrier family 6 (neurotransmitter transporter, GABA), member 1 solute carrier family 1 (high affinity glutamate transporter), member 1 neuropilin (NRP) and tollloid (TLL)-like 1 neuropilin (NRP) and tollloid (TLL)-like 2	14415 269994 232333 20510 246317 74513	Tiagabine Riluzole
G-protein coupled signaling transduction, Mapk signaling pathway	<i>Acvr1c</i> <i>Arpp21</i> <i>Arrdc4</i> <i>Crem</i> <i>Gpr176</i> <i>Gpr88</i> <i>Gps1</i> <i>Mapk14</i> <i>Ndst1</i> <i>Oprl1</i> <i>Pde10a</i> <i>Pdgfb</i> <i>Pea15a</i> <i>Prkx</i> <i>Rab14</i> <i>Rab39b</i> <i>Rcan2</i> <i>Rgs2</i> <i>Rgs6</i> <i>Rgs8</i> <i>Sirpa</i> <i>Sos1</i>	activin A receptor, type IC cyclic AMP-regulated phosphoprotein, 21 arrestin domain containing 4 cAMP responsive element modulator G protein-coupled receptor 176 G-protein coupled receptor 88 G protein pathway suppressor 1 mitogen-activated protein kinase 14 N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 opioid receptor-like 1 phosphodiesterase 10A platelet derived growth factor, B polypeptide phosphoprotein enriched in astrocytes 15A protein kinase, X-linked RAB14, member RAS oncogene family RAB39B, member RAS oncogene family regulator of calcineurin 2 regulator of G-protein signaling 2 regulator of G-protein signaling 6 regulator of G-protein signaling 8 signal-regulatory protein alpha son of sevenless homolog 1 (Drosophila)	269275 74100 66412 12916 381413 64378 209318 26416 15531 18389 23984 18591 18611 19108 68365 67790 53901 19735 50779 67792 19261 20662	
Other seizure or motor activity associated genes	<i>Car7</i> <i>Fxr2</i> <i>Sez6</i>	carbonic anhydrase 7 fragile X mental retardation, autosomal homolog 2 seizure related gene 6	12354 23879 20370	Topiramad